GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 04:37:24; Search time 1703.81 Seconds

(without alignments)

7460.491 Million cell updates/sec

(

Title: US-09-852-261-5

Perfect score: 523

Sequence: 1 ggaccggagacgctctgcgg.....aaatacacaagtaaacattc 523

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:*

1: em_estba:*

2: em esthum:*

3: em estin:*

4: em estmu:*

5: em estov:*

6: em_estpl:*

7: em_estro:*

8: em htc:*

9: gb_est1:*

10: gb est2:*

11: gb_htc:*

12: qb est3:*

13: gb est4:*

14: gb est5:*

15: em estfun:*

16: em estom:*

17: em_gss_hum:*

18: em gss inv:*

19: em gss_pln:*

20: em gss vrt:*

21: em gss fun:*

22: em gss mam:*

23: em gss mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em gss vrl:*

28: gb_gss1:* 29: gb_gss2:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

D1 +			δ •••••••				
Re	sult	0	Query	Tonath	ŊΒ	TD	Description
	No.	Score	Match	Length	םע	ID	
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c	_	363	69.4	623	9	AW146128	AW146128 um37e10.x
C		348.2	66.6	549	9	AI169253	AI169253 EST215088
C		340.2	66.3	558	9	AI265629	AI265629 uj04b07.x
С	5	339.6	64.9	614	14	CD373004	CD373004 UI-R-GR0-
	5 6	339.2	64.9	816	9	AI119218	AI119218 ue94h02.y
	7	334.8	64.0	594	10	BF383724	BF383724 602044632
	8		63.9	796	14	CB959991	CB959991 AGENCOURT
_	_	334.4	61.6	499	9	AW495481	AW495481 UI-M-BH3-
С		322.2		642	9	AI876493	AI876493 uj59b10.x
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С		305	58.3	498		AA542914	AI604642 vm43d08.y
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С		296.4	56.7	653	13	BQ200567	AA913900 ol35g05.s
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ALIGNMENTS

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DEFINITION
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ACCESSION
            AT503976.1 GI:4401827
VERSION
KEYWORDS
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            Mus musculus (house mouse)
SOURCE
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               (bases 1 to 558)
REFERENCE
            Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
  AUTHORS
            Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person
            ,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter
            ,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
            Waterston, R. and Wilson, R.
            The WashU-NCI Mouse EST Project 1999
  TITLE
            Unpublished
  JOURNAL
            Contact: Marra M/WashU-NCI Mouse EST Project 1999
COMMENT
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:565223
            This clone was previously sequenced on the 5' end only, this new
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                          133 c
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BASE COUNT
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ORIGIN

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                                                                              82: Indels
                                                                                                     7:
                                                                                                           Gaps
   Matches 441; Conservative
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QУ
                      11111 | 1111 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11
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Qy
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                   IMAGE:2247498 3' similar to gb:X04482 Mouse mRNA for
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 ACCESSION
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                   EST.
                   Mus musculus (house mouse)
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 REFERENCE
                   Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
    AUTHORS
                   Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person
```

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,B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter
           ,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
           Waterston, R. and Wilson, R.
           The WashU-NCI Mouse EST Project 1999
 TITLE
           Unpublished
 JOURNAL
           Contact: Marra M/WashU-NCI Mouse EST Project 1999
COMMENT
           Washington University School of Medicine
           4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
           Tel: 314 286 1800
           Fax: 314 286 1810
           Email: mouseest@watson.wustl.edu
           This clone is available royalty-free through LLNL; contact the
           IMAGE Consortium (info@image.llnl.gov) for further information.
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           Seg primer: custom primer used
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                   Site 2: DraIII (CACCATGTG); 1st strand cDNA was primed
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                   double-stranded cDNA was ligated to a DraIII adaptor
                   [TGTTGGCCTACTGG], digested and cloned into distinct DraIII
                   sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site
                   CACCATGTG). XhoI should be used to isolate the cDNA
                   insert. Size selection was performed to exclude fragments
                   <1.5kb. Library constructed by Dr. Sumio Sugano
                    (University of Tokyo Institute of Medical Science).
                   Custom primers for sequencing: 5' end primer
                   CTTCTGCTCTAAAAGCTGCG and 3' end primer
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                                170 g
                                        191 t
                                                  1 others
               123 a
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          Rattus.
          1 (bases 1 to 549)
REFERENCE
          Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J.,
 AUTHORS
          Kerlavage, A.R. and Adams, M.D.
          Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
 TITLE
          Gene Index
  JOURNAL
          Unpublished
          On Oct 6, 1998 this sequence version replaced gi:3705561.
COMMENT
          Other ESTs: TC50779
          Contact: Lee, NH
          The Institute for Genomic Research
          9712, Medical Center Drive, Rockville, MD 20850, USA
          Tel: (301)-838-3529
          Fax: (301)-838-0208
          Email: nhlee@tigr.org
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 Best Local Similarity
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                              558 bp
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DEFINITION
         IMAGE: 1890901 3' similar to gb: X04482 Mouse mRNA for
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ACCESSION
         AI265629
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KEYWORDS
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            Mus musculus (house mouse)
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            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
               (bases 1 to 558)
REFERENCE
            Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
 AUTHORS
            Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
            Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
            Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
            Waterston, R.
            The WashU-HHMI Mouse EST Project
 TTTLE
            Unpublished
  JOURNAL
            Contact: Marra M/Mouse EST Project
COMMENT
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
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                     (CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
                     was primed with an oligo(dT) primer
                     [ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
                     ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
                     and cloned into distinct DraIII sites of the pME18S-FL3
                     vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
                     be used to isolate the cDNA insert. Size selection was
                     performed to exclude fragments <1.5kb. Library
                     constructed by Dr. Sumio Sugano (University of Tokyo
                     Institute of Medical Science). Custom primers for
                     sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
                     primer CGACCTGCAGCTCGAGCACA."
BASE COUNT
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                         135 c
                                  156 g
                                            161 t
ORIGIN
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  Query Match
                          82.0%; Pred. No. 2.5e-76;
  Best Local Similarity
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0; Mismatches

Matches 414; Conservative

85; Indels

6; Gaps

AI265629.1 GI:3883787

VERSION

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Qу
           15111 15111 11 11511 11551 1551 1551 1551 1551 1551 1551 1551 1551 1551 1551 1551
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Db
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Db
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Qу
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Db
        Qу
           326 TGTGCCCCACTGAAGCCTACAAAAGCAGCCCGCTCTATCCGTGCCCAGCGCCACACTGAC 267
Db
        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
Qy
           Db
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Db
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Qу
           1[1 ][1][1][1] [1] [1] [1]
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Db
        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA----AAAAATAAGTTTGATC 474
Qу
                          111111 1 11 111 111
                                                11 1111111
                      1
           | \cdot |
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Db
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Qy
           11 1111
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                              614 bp
                                       mRNA
LOCUS
          CD373004
          UI-R-GRO-csv-j-17-0-UI.rl UI-R-GRO Rattus norvegicus cDNA clone
DEFINITION
          UI-R-GRO-csv-j-17-0-UI 5', mRNA sequence.
          CD373004
ACCESSION
          CD373004.1 GI:31157094
VERSION
KEYWORDS
          EST.
SOURCE
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          Rattus norvegicus
 ORGANISM
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
          Rattus.
REFERENCE
            (bases 1 to 614)
          Bonaldo, M.F., Lennon, G. and Soares, M.B.
 AUTHORS
          Normalization and subtraction: two approaches to facilitate gene
  TITLE
          discovery
          Genome Res. 6 (9), 791-806 (1996)
  JOURNAL
 MEDLINE
          97044477
  PUBMED
          8889548
```

```
Contact: Soares, MB
COMMENT
           Coordinated Laboratory for Computational Genomics
           University of Iowa
           375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
           Tel: 319 335 8250
           Fax: 319 335 9565
           Email: bento-soares@uiowa.edu
           Tissue Procurement: James Lin, University of Iowa
            cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Distribution information can be found at
           http://genome.uiowa.edu/distribution/rat.html
           Seg primer: M13 REVERSE.
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                   /lab host="DH10B (Life Technologies) (T1 phage resistant)"
                   /clone lib="UI-R-GR0"
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                   tissue(s): rat whole embryo 13dpc. The library was
                   constructed according to Bonaldo, Lennon and Soares,
                   Genome Research, 6:791-806, 1996. Denatured RNA was size
                   fractionated on a 1% agarose gel. First strand cDNA
                   synthesis was primed with oligo-dT primer containing a Not
                   I site. Double strand cDNA was size selected according to
                   mRNA size fraction, ligated with EcoR I adaptor, digested
                   with NotI and then cloned directionally into pYX-Asc
                   vector. The library tag sequence located between the Not I
                   site and the polyA tail is CATCTCTACT. This library was
                   created for the University of Iowa Program for Rat Gene
                   Discovery and Mapping (Val Sheffield, Bento Soares and Tom
                   Casavant)."
                       168 c
                               154 g
                                        119 t
                                                  2 others
BASE COUNT
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ORIGIN
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                        81.4%; Pred. No. 1.9e-74;
  Best Local Similarity
  Matches 393; Conservative
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                                                   Indels
                                                             0; Gaps
                                                                        0;
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Qу
            \perp
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Db
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Qу
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                       ł
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Db
         481 CAA 483
Qу
            1 1
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RESULT 6
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                                816 bp
LOCUS
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          IMAGE:1498803 5' similar to qb:X04482 Mouse mRNA for
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          AI119218
ACCESSION
          AI119218.1 GI:3519542
VERSION
KEYWORDS
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SOURCE
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          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
             (bases 1 to 816)
REFERENCE
          Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
 AUTHORS
          Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
          Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
          Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
          Waterston, R.
          The WashU-HHMI Mouse EST Project
  TITLE
          Unpublished
  JOURNAL
          Contact: Marra M/Mouse EST Project
COMMENT
          WashU-HHMI Mouse EST Project
          Washington University School of MedicineP
          4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
          Tel: 314 286 1800
          Fax: 314 286 1810
          Email: mouseest@watson.wustl.edu
          This clone is available royalty-free through LLNL; contact the
          IMAGE Consortium (info@image.llnl.gov) for further information.
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MGI:936407
Seq primer: custom primer used
High quality sequence stop: 473.

FEATURES
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Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed
with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTTTT];
double-stranded cDNA was ligated to a DraIII adaptor
[TGTTGGCCTACTGG], digested and cloned into distinct DraIII
sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site
CACCATGTG). XhoI should be used to isolate the cDNA
insert. Size selection was performed to exclude fragments
<1.5kb. Library constructed by Dr. Sumio Sugano
(University of Tokyo Institute of Medical Science).
Custom primers for sequencing: 5' end primer
CTTCTGCTCTAAAAGCTGCG and 3' end primer

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Qу	61	AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG	120
Db	383	AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCTCAG	442
Qу	121	ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC	180
Db	443	ACAGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGACTGGAGATGTAC	502
Qу	181	TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCG	240
Db	503	TGTGCCCCACTGAAGCCTACAAAAGCAGCCCGCTCTATCCGTGCCCAGCGCCACACTGAC	562
QУ	241	ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG	300
Db	563	ATGCCCAAGACTCAGAAGTCCCCGTCCCTATCGACAAACAA	622
Qу	301	AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA	360
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Qу
             111111 11 11 11111
         683 CAGAATGTANGAGGAGCCTNCCACGGAGCAGAANATGCCACATCACCGCANGATCCTTTG 742
Db
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Db
RESULT 7
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LOCUS
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DEFINITION
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ACCESSION
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           BF383724.1 GI:11365029
VERSION
KEYWORDS
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SOURCE
           Mus musculus
 ORGANISM
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           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              (bases 1 to 594)
REFERENCE
           NIH-MGC http://mgc.nci.nih.gov/.
 AUTHORS
           National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE
           Unpublished
 JOURNAL
           Contact: Robert Strausberg, Ph.D.
COMMENT
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Jeffrey E. Green, M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
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BASE COUNT
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                                                                   Gaps
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Qу		TGTGATCTGAGGAGGCTGGAGATGTA	
Db		CTGTGATCTGAGGAGACTGGAGATGTA	
Qу		TCCGTCCGTGCCCAGCGCCACACCG	
Db		CTCTATCCGTGCCCAGCGCCACACTGA	
QУ		PACCAACAAGAAAATGAAGTCTCAGAG	
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Qу		GTAGAGGGAGTGCAGGAAACAAGAACT	
Db			
Qу		SAAGGACAGGCCACCGCAGGACCCTTT	
Db		AAATGCCACATCACCGCAGGATCCTTI	GCTGCTTGAGCAACCT 526
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	and advice from Pie		(mileta)

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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Agencourt Bioscience Corporation
          Clone distribution: MGC clone distribution information can be
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         http://image.llnl.gov
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                 /clone lib="NIH MGC 147"
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                 insert size 2.3 kb and normalized to ROT 5. This is a
                 primary library enriched for full-length clones and
                 constructed using the Cap-trapper method (Carninci, in
                 preparation). Library constructed by M. Brownstein
                 (NIMH/NHGRI, National Institutes of Health). Note: This is
                 a NIH MGC library."
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                                   184 t
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                                             Indels
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Qу
           180 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGGAGAC 239
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Db
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Qу
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ACCESSION
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VERSION
KEYWORDS
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           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              (bases 1 to 499)
REFERENCE
           Bonaldo, M.F., Lennon, G. and Soares, M.B.
 AUTHORS
           Normalization and subtraction: two approaches to facilitate gene
 TITLE
           discovery
           Genome Res. 6 (9), 791-806 (1996)
  JOURNAL
           97044477
 MEDLINE
           8889548
  PUBMED
COMMENT
           Contact: Chin, H
           National Institute of Mental Health
           6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
           20892-9643, USA
           Tel: 301 443 1706
           Fax: 301 443 9890
           Email: mEST@mail.nih.gov
           The sequence contained an oligo-dT track that was present in the
           oligonucleotide that was used to prime the synthesis of first
           strand cDNA and therefore this may represent a bonafide poly A
           tail. The sequence tag present in the cDNA between the NotI site
           and the oligo-dT track served to identify it as a clone from the
           normalized pineal glands library cDNA Library Preparation: M.B.
           Soares Lab Clone distribution: Researchers may obtain BMAP cDNA
           clones from RESEARCH GENETICS. It should be noted that Bento Soares
           is generating a small number of additional specialized
           non-redundant arrays of BMAP cDNAs whose availability will be
           considered under appropriate and limited collaborative arrangements
           Seg primer: M13 Forward
           POLYA=Yes.
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                ultimately derived from a mixture of individually tagged
                normalized libraries from ten regions of the mouse brain
                 (cerebellum, brain stems, olfactory bulbs, hypothalamus,
                 cortex, amygdala, basal ganglia, pineal gland, striatum,
                hipoccampus) after a series of subtractions to reduce the
                 representation of cDNAs from which ESTs had already been
                generated. The following serially subtracted libraries
                were generated in this process: NIH BMAP M S4,
                NIH BMAP M S3.3, NIH BMAP M S3.2, NIH BMAP M S3.1,
                NIH BMAP M S2, NIH BMAP M S1. The subtracted library
                 (NIH BMAP M S4) was constructed as follows: PCRamplified
                 cDNA inserts from NIH BMAP M S3.3, NIH BMAP M S3.2, and
                NIH BMAP M S3.1 clones from which 3' ESTs had been derived
                was used as a driver in a hybridization with a pool of
                 the NIH BMAP M S3.3, NIH BMAP M S3.2, and NIH BMAP M S3.1
                libraries in the form of single-stranded circles. The
                 remaining single-stranded circles (subtracted library)
                was purified by hydroxyapatite column chromatography,
                 converted to double-stranded circles and electroporated
                into DH10B bacteria (LifeTechnologies) to generate the
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                TAG SEQ=CAGAC"
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                            124 q
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Best Local Similarity
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Matches 396; Conservative
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                                               Indels
                                                        7; Gaps
                                                                   2;
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                    499 TGTGTGGACCGAGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGA 440
       110 GGGCACCTCAGACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGC 169
          439 GGGCACCTCAGACAGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGAC 380
       379 TGGAGATGTACTGTGCCCCACTGAAGCCTACAAAAGCAGCCCGCTCTATCCGTGCCCAGC 320
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230 GCCACACCGACATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGA 289

290 AGTCTCAGAGGAGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGA 349

BASE COUNT

Query Match

ORIGIN

Qy

Db

Qу

Db

Qу

Db

Qу

Db

Qу

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259 AGCTGCAAAGGAGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGAAGTGCAGGA 200
Db
         350 AACAAGAACTACAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGC 409
Qу
             1 11 1 11
         199 AACAAGACCTACAGAATGTAGGAGGAGCCTCCCACGGAGCAGAAAATGCCACATCACCGC 140
Db
         410 AGGACCCTTTGCTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA-----AAAAA 463
Qу
             1111 1111111
                                        -1
         139 AGGATCCTTTGCTGCTTGAGCAACCTGCAAAACATCGAAACACCTACCAAATAACAATAA 80
Db
         464 TAAGTTTGATCACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATT 522
Qу
                    79 TAAGTCCAATAACATTACAAGATGGGCATTTCCCCCAATGAAATATACAAGTAAACATT 20
Db
         523 C 523
Qу
          19 C 19
Db
RESULT 10
AI876493/c
                                  642 bp
                                           mRNA
                                                   linear
                                                            EST 21-JUL-1999
LOCUS
           AI876493
          uj59b10.x1 Sugano mouse liver mlia Mus musculus cDNA clone
DEFINITION
           IMAGE: 1924219 3' similar to gb: X57025 rna1 INSULIN-LIKE GROWTH
           FACTOR IA PRECURSOR (HUMAN); gb:X04482 Mouse mRNA for
           preproinsulin-like growth factor IB (MOUSE);, mRNA sequence.
ACCESSION
           AI876493
           AI876493.1 GI:5550542
VERSION
           EST.
KEYWORDS
           Mus musculus (house mouse)
SOURCE
 ORGANISM Mus musculus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
           1 (bases 1 to 642)
REFERENCE
           Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
 AUTHORS
           Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person
           ,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter
           ,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
           Waterston, R. and Wilson, R.
           The WashU-NCI Mouse EST Project 1999
 TITLE
 JOURNAL
           Unpublished
           Contact: Marra M/WashU-NCI Mouse EST Project 1999
COMMENT
           Washington University School of Medicine
           4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
           Tel: 314 286 1800
           Fax: 314 286 1810
           Email: mouseest@watson.wustl.edu
           This clone is available royalty-free through LLNL; contact the
           IMAGE Consortium (info@image.llnl.gov) for further information.
           MGI:980511
           Seq primer: custom primer used
           High quality sequence stop: 257.
FEATURES
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                   1. .642
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                /clone="IMAGE:1924219"
                /sex="female"
                /dev stage="adult"
                /lab host="DH10B"
                /clone lib="Sugano mouse liver mlia"
                /note="Organ: liver; Vector: pME18S-FL3; Site_1: DraIII
                 (CACTGTGTG); Site 2: DraIII (CACCATGTG); 1st strand cDNA
                was primed with an oligo(dT) primer
                 [ATGTGGCCTTTTTTTTTTTTTTT]; double-stranded cDNA was
                ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
                and cloned into distinct DraIII sites of the pME18S-FL3
                vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
                be used to isolate the cDNA insert. Size selection was
                performed to exclude fragments <1.5kb. Library
                constructed by Dr. Sumio Sugano (University of Tokyo
                Institute of Medical Science). Custom primers for
                sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
                primer CGACCTGCAGCTCGAGCACA."
BASE COUNT
            127 a
                   154 c
                           175 q
                                  185 t
                                           1 others
ORIGIN
                           Score 320.8; DB 9; Length 642;
 Query Match
                    61.3%;
 Best Local Similarity
                    80.1%;
                          Pred. No. 9.6e-70;
 Matches 403; Conservative
                          0: Mismatches
                                        93;
                                           Indels
                                                    7;
                                                       Gaps
                                                             2;
         2 GACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGACA 61
Qу
           Db
        503 GACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGATGCTCTTCAGGTCGTGTGTGGACCGA 444
        62 GGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAGA 121
Qу
                   Db
        443 GGGGCTTTTTCTTCAACAAGGCCACAGGCTATGGCTCCAGCATTTGGAGGGCACCTCAGA 384
        122 CAGGCATCGTGGATGAGTGCTGCTTCCGG-AGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
Qy
           383 CAGTCAATGTGGATGAGTGTTGCTTCCGGAAGCTGTGATCTGAGAAGACTGNAGATGTAC 324
Db
       Qу
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Db
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Qу
           Db
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301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360

361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420

143 CAGAATGTAGGAGGAGCCTCCCACGGAGCAGAAAATGCCACATCACCGCAGGATCCTTTG 84

421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA-----AAAAATAAGTTTGATC 474

Qy

Db

Qу

Db

Qу

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83 CTGCTTGAGCAACCTGCAAAACATCGAAACACCTACCAAATAACAATAATAAGTCCAATA 24
Db
          475 ACATTTCAAAGATGGCATTTCCC 497
Qу
              1111 11111111
                               11 11
           23 ACATTACAAAGATGGGCATTTCC 1
Dh
RESULT 11
BM984670/c
                                                                 EST 20-FEB-2003
                                                       linear
                                     673 bp
                                               mRNA
LOCUS
            BM984670
           UI-CF-EC1-abj-k-24-0-UI.sl UI-CF-EC1 Homo sapiens cDNA clone
DEFINITION
            UI-CF-EC1-abj-k-24-0-UI 3', mRNA sequence.
            BM984670
ACCESSION
            BM984670.1 GI:19610417
VERSION
KEYWORDS
            EST.
            Homo sapiens (human)
SOURCE
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 673)
REFERENCE
            Bonaldo, M.F., Lennon, G. and Soares, M.B.
  AUTHORS
            Normalization and subtraction: two approaches to facilitate gene
  TITLE
            discovery
            Genome Res. 6 (9), 791-806 (1996)
  JOURNAL
            97044477
  MEDLINE
            8889548
   PUBMED
            Contact: McCray, PB
COMMENT
            McCray Lab
            University of Iowa
            2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
            Tel: 319 356 4866
            Fax: 319 356 7171
            Email: paul-mccray@uiowa.edu
            Tissue Procurement: Dr. M. J. Welsh, University of Iowa
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com) or from Open Biosystems
            (www.openbiosystems.com).
            Seg primer: M13 FORWARD
            POLYA=Yes.
                     Location/Qualifiers
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                     /tissue type="Lung"
                     /dev stage="Adult and Fetal"
                     /lab host="DH10B (Life Technologies) (T1 phage resistant)"
                     /clone lib="UI-CF-EC1"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     UI-CF-EC1 is a normalized cDNA library containing the
                     following tissue(s): Normal lung from adult and from fetal
                     day 64, day 87, week 19 and week 42. The library was
```

constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AAGTGCTTAC.

TAG LIB=UI-CF-EC1

TAG_TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371 and 380-383

5 :

TAG_SEQ=AAGTGCTTAC"

BASE COUNT ORIGIN 152 a 164 c 169 g 188 t

Query Match 61.3%; Score 320.8; DB 12; Length 673;
Best Local Similarity 84.2%; Pred. No. 9.7e-70;
Matches 443: Conservative 0: Mismatches 27: Indels 56: Gaps

Matches	443	; Conservative 0; Mism	natches	27;]	Indels	56;	Gaps	5;
Qу	1	GGACCGGAGACGCTCTGCGGTGCTGAG						60
Db	492	GGACCGGAGACGCTCTGCGGGGCTGAC						433
Qу	61	AGGGGCTTTTATTTCAACAAGCCCACA						120
Db	432	AGGGG-TTTTATTTCAGCAAGCCCACA						374
Qу	121	ACAGGCATCGTGGATGAGTGCTGCTTC						180
Db	373	ACAGGCATCGTGGATGAGTGCTGCTTC						314
QУ	181	TGTGCACCCTCAAGCCGGCAAAGGCA						240
Db	313	TGCGCACCCCTCAAGCCTGCCAAGTCA						254
QУ	241	ATGCCCAAGACTCAGAAGTATCAGCCT	CCATCTACC	AACAA	GAAAATGAA	AGTCTO	CAGAGG	300
Db	253	ATGCCCAAGACCCAG					-	239
QУ	301	AGAAGGAAAGGAAGTACATTTGAAGAA						360
Db	238	AAGGAAGTACATTTGAAGAA						186
Qу	361	CAGGATGTAGGAAGACCCTTCTGAGGA						420
Db	185	CAGGATGTAGGAAGACCCTCCTGAGGA						126
Qу	421	CTCTGCAC-AGTTACCTG-TAAACAT						478
Db	125	CTCTGCACGAGTTACCTGTTAAACTT						66
Qу	479	TTCAAAGAT-GGCATTTCCCCCAATGA				3		
Db	65	TTAAAAGATGGGCGTTTCCCCCAATGA						

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RESULT 12
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                                                             EST 01-DEC-1998
                                                     linear
           AI248089
                                   575 bp
                                             mRNA
LOCUS
           qh69f05.xl Soares fetal_liver spleen_1NFLS S1 Homo sapiens cDNA
DEFINITION
           clone IMAGE:1849953 3' similar to gb:X57025 rnal INSULIN-LIKE
           GROWTH FACTOR IA PRECURSOR (HUMAN);, mRNA sequence.
           AI248089
ACCESSION
           AI248089.1 GI:3843486
VERSION
           EST.
KEYWORDS
           Homo sapiens (human)
SOURCE
           Homo sapiens
  ORGANISM
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
              (bases 1 to 575)
           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 AUTHORS
           National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 TITLE
           Tumor Gene Index
  JOURNAL
           Unpublished
COMMENT
           Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           This clone is available royalty-free through LLNL; contact the
           IMAGE Consortium (info@image.llnl.gov) for further information.
           Insert Length: 918
                               Std Error: 0.00
           Seq primer: -40UP from Gibco
           High quality sequence stop: 380.
                    Location/Qualifiers
FEATURES
                    1. .575
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                    /dev stage="20 week-post conception fetus"
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                    /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
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                    This is a subtracted version of the original Soares fetal
                                                 1st strand cDNA was primed
                    liver spleen 1NFLS library.
                    with a Pac I - oligo(dT) primer [5'
                    double-stranded cDNA was ligated to Eco RI adaptors
                    (Pharmacia), digested with Pac I and cloned into the Pac I
                    and Eco RI sites of the modified pT7T3 vector. Library
                    went through one round of normalization. Library
                    constructed by Bento Soares and M. Fatima Bonaldo."
                                 131 g
                                         156 t
                                                    1 others
BASE COUNT
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                         83.8%; Pred. No. 9.4e-69;
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                                                              55;
                                                                          4;
  Matches 428; Conservative
                                0; Mismatches
                                                28;
                                                     Indels
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Qy
             551 TGCGGGGCTGAGCTGGTGNATGCTCTTCAGTTCGTGTGAAGACAGGGGCTTTTATTTC 492
Db
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Qy	76 AACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAGACAGGCATCGTGGAT 135
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Qy	136 GAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTACTGTGCACCCCTCAAG 195
Db	431 GAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTATTGCGCACCCCTCAAG 372
Qy	196 CCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGACATGCCCAAGACTCAG 255
Db	371 CCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGACATGCCCAAGACCCAG 312
Qу	256 AAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGGAGAAGGAAAGGAAGT 315
Db	311AAGGAAGT 304
Qу	316 ACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAGGATGTAGGAAGA 375
Db	303 ACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAGGATGTAGGAAGA 244
Qу	376 CCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCTCTGCAC-AGTTAC 434
Db	243 CCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTGCTCTGCACGAGTTAC 184
Qy	435 CTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTTCAAAGAT-GGCAT 492
Db	183 CTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACATTTAAAAGATGGGCGT 124
Qу	493 TTCCCCCAATGAAATACACAAGTAAACATTC 523
Db	
RESULT 13 A1169770/LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISE	AI169770 468 bp mRNA linear EST 20-JAN-1999 N EST215669 Normalized rat liver, Bento Soares Rattus sp. cDNA clone RLIAT07 3' end, mRNA sequence. AI169770 AI169770.1 GI:3709810 EST. Rattus sp. Rattus sp. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. 1 (bases 1 to 468)
AUTHORS TITLE	Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J., Kerlavage, A.R. and Adams, M.D. Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
	Gene Index
JOURNAL COMMENT	Other_ESTs: TC50779 Contact: Lee, NH The Institute for Genomic Research
	9712, Medical Center Drive, Rockville, MD 20850, USA

```
Tel: (301)-838-3529
         Fax: (301)-838-0208
         Email: nhlee@tigr.org
         Seq primer: M13-21.
                Location/Qualifiers
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                Site 2: NotI"
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BASE COUNT
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 Query Match
 Best Local Similarity 81.8%; Pred. No. 7.2e-67;
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 Matches 383; Conservative
                          0; Mismatches
                                       78;
                                            Indels
                                                    7:
                                                       Gaps
         63 GGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAGAC 122
Qу
           468 GGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCACAGAC 409
Db
        123 AGGCATCGTGGATGATGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTACTG 182
Qy
            408 GGGCATTGTGGATGAGTGTTGCTCCCGGAGCTGTGATCTGAGGAGGTTGGAGATGTACTG 349
Db
        183 TGCACCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGACAT 242
Qу
           348 TGCTCCGCTGAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGACAT 289
Db
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Qy
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Qу
           228 AAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTACA 169
Db
        363 GGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCT 422
Qу
           168 GAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTGCT 109
Db
        423 CTGCACAGTTACCTGTAAACATTGGAATACCGGCCA-----AAAAATAAGTTTGATCAC 476
Qу
                       1
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Qу
           48 ATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTC 1
Db
RESULT 14
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AA542914/c

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DEFINITION
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            (HUMAN);, mRNA sequence.
            AA542914
ACCESSION
            AA542914.1 GI:2291394
VERSION
            EST.
KEYWORDS
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SOURCE
           Homo sapiens
  ORGANISM
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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            1 (bases 1 to 498)
REFERENCE
           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 AUTHORS
           National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 TITLE
            Tumor Gene Index
            Unpublished
  JOURNAL
            Contact: Robert Strausberg, Ph.D.
COMMENT
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 603
                               Std Error: 0.00
            Seq primer: -40ml3 fwd. ET from Amersham
            High quality sequence stop: 412.
                     Location/Qualifiers
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                     /clone="IMAGE: 984882"
                     /sex="male"
                     /tissue type="normal prostate"
                     /lab host="DH10B"
                     /clone lib="NCI CGAP Pr21"
                     /note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
                     with a modified polylinker; 1st strand cDNA was prepared
                     from normal prostate bulk tissue, and was then primed with
                     a Not I - oligo(dT) primer. Double-stranded cDNA was
                     ligated to Eco RI adaptors (Pharmacia), digested with Not
                     I and cloned into the Not I and Eco RI sites of the
                     modified pT7T3 vector. Library is not normalized. Library
                     was constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT
                105 a
                         135 с
                                  123 q
                                           135 t
ORIGIN
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  Best Local Similarity
                          83.5%; Pred. No. 8.2e-66;
                                 0; Mismatches
                                                  30; Indels
                                                                57; Gaps
                                                                             6:
  Matches 440; Conservative
            1 GGACCGGAGACGCTCTGCGGTGC-TGAGCTGGTGGATGCTCTTCAGTTCGTGTGGAGA 59
Qу
                          476 GGACCGGAGAACTTTTGCGGGGCTTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGA 417
Db
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Qy	60 CAGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCA 119
Db	
Qу	120 GACAGGCATCGTGGATGAGTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTA 179
Db	
QУ	180 CTGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCG
Db	297 TTGCGCACCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGA 238
Qу	240 CATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAG 299
Db	237 CATGCCCAAGACCCAG 222
Qу	300 GAGAAGGAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACT 359
Db	221AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACT 170
QУ	360 ACAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTT 419
Db	169 ACAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTT 110
QУ	420 GCTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACA 477
Db	109 GCTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACA 50
Qу	478 TTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
Db	49 TTTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTC 3
RESULT 15 AI604642 LOCUS DEFINITIO	clone IMAGE:1001007 5' similar to gb:M11568 INSULIN-LIKE GROWTH FACTOR IB PRECURSOR (HUMAN); gb:X04482 Mouse mRNA for
ACCESSION VERSION KEYWORDS SOURCE ORGANIS	preproinsulin-like growth factor IB (MOUSE);, mRNA sequence. AI604642 AI604642.1 GI:4613809 EST. Mus musculus (house mouse) Mus musculus
REFERENCE AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 882) Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
TITLE JOURNAL COMMENT	Waterston,R. and Wilson,R. The WashU-NCI Mouse EST Project 1999 Unpublished Contact: Marra M/WashU-NCI Mouse EST Project 1999 Washington University School of Medicine

```
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
         Tel: 314 286 1800
          Fax: 314 286 1810
          Email: mouseest@watson.wustl.edu
         This clone is available royalty-free through LLNL; contact the
          IMAGE Consortium (info@image.llnl.gov) for further information.
         MGI:565223
         This read is a RESEQUENCE of a previously sequenced mouse clone
          This read has been verified (found to hit its original self in the
          correct orientation)
          Seq primer: -40RP from Gibco
          High quality sequence stop: 361.
                 Location/Qualifiers
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Job time : 1704.81 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 05:41:20; Search time 2336.77 Seconds

(without alignments)

9156.102 Million cell updates/sec

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Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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2	523	100.0	523	6	AX300783	AX300783 Sequence
3	467.4	89.4	517	6	AX147742	AX147742 Sequence
4	467.4	89.4	517	6	AX300779	AX300779 Sequence
5	409	78.2	471	6	AX147754	AX147754 Sequence
6	409	78.2	471	6	AX300791	AX300791 Sequence
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8	361.6	69.1	798	10	RNIGFI2	X06108 Rat mRNA (c
9	361.6	69.1	958	10	RNIGFI1	X06107 Rat mRNA (c
10	358.4	68.5	710	10	RATIGFIA	M15480 Rat insulin
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ACCESSION
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VERSION
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REFERENCE
  AUTHORS
            Goldspink, G.R. and Johnson, I.R.
  TITLE
            Use of the insulin-like-growth factor i isoform mgf for the
            treatment of neurological disorders
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REFERENCE
         Goldspink, G.D. and Terenghi, G.B.
 AUTHORS
         Repair of nerve damage
 TITLE
         Patent: WO 0185781-A 5 15-NOV-2001;
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         University College London (GB) ; East Grinstead Medical Research
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REFERENCE
         Goldspink, G.R. and Johnson, I.R.
 AUTHORS
 TITLE
         Use of the insulin-like-growth factor i isoform mgf for the
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         Patent: WO 0136483-A 1 25-MAY-2001;
 JOURNAL
         University College London (GB)
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REFERENCE
          Goldspink, G.D. and Terenghi, G.B.
 AUTHORS
          Repair of nerve damage
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REFERENCE
 AUTHORS
         Goldspink, G.R. and Johnson, I.R.
         Use of the insulin-like-growth factor i isoform mgf for the
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REFERENCE
 AUTHORS
        Goldspink, G.D. and Terenghi, G.B.
 TITLE
        Repair of nerve damage
 JOURNAL,
        Patent: WO 0185781-A 13 15-NOV-2001;
        University College London (GB); East Grinstead Medical Research
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                                     1536 bp
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DEFINITION
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            MGC:18617 IMAGE:4194295), complete cds.
            BC012409
ACCESSION
            BC012409.1 GI:15214568
VERSION
KEYWORDS
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SOURCE
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REFERENCE
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 AUTHORS
            Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
            Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
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            Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
            Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
            Generation and initial analysis of more than 15,000 full-length
 TITLE
            human and mouse cDNA sequences
            Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  JOURNAL
 MEDLINE
            22388257
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   PUBMED
            2 (bases 1 to 1536)
REFERENCE
            Strausberg, R.
 AUTHORS
  TITLE
            Direct Submission
            Submitted (15-AUG-2001) National Institutes of Health, Mammalian
  JOURNAL
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
            NIH-MGC Project URL: http://mgc.nci.nih.gov
  REMARK
COMMENT
            Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Baylor College of Medicine Human Genome
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Center code: BCM-HGSC
          Web site: http://www.hgsc.bcm.tmc.edu/cdna/
          Contact: amg@bcm.tmc.edu
          Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
          Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
          A.N., Gibbs, R.A.
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Sequencing Center

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DEFINITION Rat mRNA (clone IGF1AB2) for insulin-like growth factor I.
ACCESSION
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VERSION
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KEYWORDS
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          Rattus.
REFERENCE
          1
          Shimatsu, A. and Rotwein, P.
 AUTHORS
          Sequence of Two Rat Insulin-like Growth Factor I mRNAs Differing
 TITLE
          Within the 5' Untranslated Region
          Nucleic Acids Res. 15 (1987) In press
 JOURNAL
            (bases 1 to 798)
REFERENCE
          2
 AUTHORS
          Rotwein, P.
 TITLE
          Direct Submission
          Submitted (21-OCT-1987) Rotwein P., Washington University, School
 JOURNAL
          of Medicine, 660 South Euclid Avenue, Box 8127, St. Louis, MO
          63110, USA
          Another IGF-I mRNA of rat liver differing in the 5' UT-region is
COMMENT
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VERSION
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REFERENCE
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  AUTHORS
           Shimatsu, A. and Rotwein, P.
            Sequence of two rat insulin-like growth factor I mRNAs differing
  TITLE
           within the 5' untranslated region
           Nucleic Acids Res. 15 (17), 7196 (1987)
  JOURNAL
           88015572
  MEDLINE
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   PUBMED
               (bases 1 to 958)
REFERENCE
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           Rotwein, P.
  AUTHORS
           Direct Submission
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  JOURNAL
            of Medicine, 660 South Euclid Avenue, Box 8127, St. Louis, MO
            63110, USA
            Another IGF-I mRNA of rat liver differing in the 5' UT-region is
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Rattus norvegicus (Norway rat)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 710)
Roberts, C.T. Jr., Lasky, S.R., Lowe, W.L. Jr., Seaman, W.T. and LeRoith, D.
Molecular cloning of rat insulin-like growth factor I complementary deoxyribonucleic acids: differential messenger ribonucleic acid processing and regulation by growth hormone in extrahepatic tissues
Mol. Endocrinol. 1 (3), 243-248 (1987)
88288198
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Original source text: Rat (Sprague-Dawley) adult liver cDNA to mRNA, clone pRIGF-1-42.
Draft entry and computer-readable copy of sequence in [Mol. Endocrinol. (1987) In press] kindly

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provided by S.R.Lasky, 16-MAR-1987.
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VERSION
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REFERENCE
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 AUTHORS
           Goldspink, G.R. and Johnson, I.R.
           Use of the insulin-like-growth factor i isoform mgf for the
 TITLE
           treatment of neurological disorders
           Patent: WO 0136483-A 3 25-MAY-2001;
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REFERENCE
         Goldspink, G.D. and Terenghi, G.B.
 AUTHORS
 TITLE
         Repair of nerve damage
         Patent: WO 0185781-A 3 15-NOV-2001;
 JOURNAL
         University College London (GB); East Grinstead Medical Research
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DEFINITION Mouse mRNA for preproinsulin-like growth factor IB.

ACCESSION X04482

VERSION X04482.1 GI:51806

KEYWORDS growth factor; insulin-like growth factor IB; preproinsulin-like

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REFERENCE
               (bases 1 to 651)
  AUTHORS
            Bell, G.I., Stempien, M.M., Fong, N.M. and Rall, L.B.
  TITLE
            Sequences of liver cDNAs encoding two different mouse insulin-like
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  JOURNAL
           Nucleic Acids Res. 14 (20), 7873-7882 (1986)
  MEDLINE
            87040760
   PUBMED
            3774549
           The sequence is identical to the preproIGF-IA sequence (X04480)
COMMENT
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        Baak, J. and Mutter, G.L.
 TITLE
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

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28	273.6	52.3	612	22	AAS14695	Human cDNA encodin
29	273.6	52.3	612	25	ABZ83309	Toxicologically re
30	266.8	51.0	1052	20	AAX27498	Rat liver form of
31	262	50.1	487	22	AAD06404	Rat liver-type IGF
32	262	50.1	487	24	AAS16883	Rat insulin-like g
33	250	47.8	671	24	ABT09479	Phase-1 Rat CT gen
34	237.6	45.4	317	24	AAS16882	Human insulin-like
35	237.6	45.4	318	22	AAD06403	Human liver-type I
36	237.6	45.4	462	19	AAV50426	Human IGF-1 encodi
37	237.6	45.4	462	19	AAV40794	Human IGF-I coding
38	237.6	45.4	462	24	ABZ35734	Human IGF1 polynuc
39	237.6	45.4	462	24	ABX09977	Human IGF1 DNA fra
40	237.6	45.4	462	24	ABV78158	Human IGF1 DNA SEQ
41	237.6	45.4	462	24	ABL91699	Human polynucleoti
42	209	40.0	286	25	ABV76186	Mouse insulin-like
43	193	36.9	210	24	AAD45568	Human insulin-like
44	193	36.9	210	24	AAD44955	Human insulin grow
45	193	36.9	210	24	ABA03146	Native mature IGF-

```
RESULT 1
AAD06400
     AAD06400 standard; cDNA; 523 BP.
ID
XX
AC
     AAD06400;
XX
DΤ
     10-AUG-2001 (first entry)
XX
DE
     Rabbit IGF-I isoform mechano-growth factor (MGF) cDNA.
XX
KW
     Rabbit; IGF-I isoform; Insulin-like Growth Factor-I; MGF;
     mechano-growth factor; neurological disorder; neurodegenerative disorder;
KW
     amyotrophic lateral sclerosis; spinal muscular atrophy; muscular atrophy;
KW
     poliomyelitis; post-polio syndrome; toxin; motoneurone disorder;
KW
     nerve damage; autosomal muscular dystrophy; diabetic neuropathy;
KW
     sex-linked muscular dystrophy; peripheral neuropathy;
KW
     Alzheimer's disease; Parkinson's disease; ss.
KW
XX
OS
    Oryctolagus cuniculus.
XX
                     Location/Qualifiers
FH
     Key
FT
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                     1..336
FΤ
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FT
                     /product= "Mechano-growth factor (MGF)"
FT
                     /note= "This region comprises exons 3-6. The CDS does
FT
                     not include start codon"
FT
                     /partial
XX
PΝ
    WO200136483-A1.
XX
     25-MAY-2001.
PD
XX
     15-NOV-2000; 2000WO-GB04354.
PF
XX
     15-NOV-1999;
                    99GB-0026968.
PR
XX
     (UNLO ) UNIV COLLEGE LONDON.
PA
XX
PΙ
    Goldspink G, Johnson I;
XX
    WPI; 2001-355620/37.
DR
    P-PSDB; AAE02449.
DR
XX
     Use of mechano-growth factor, an isoform of Insulin-like Growth
PT
     Factor-I, capable of reducing motoneurone loss, in the manufacture of a
PT
    medicament for the treatment of neurological disorder -
PT
XX
PS
    Claim 4; Page 53-54; 66pp; English.
XX
    The present invention relates to use of mechano-growth factor (MGF),
CC
CC
     an Insulin-like Growth Factor-I (IGF-I) isoform in the manufacture of a
CC
    medicament for the treatment of neurological disorder. The MGF is capable
CC
     of reducing motoneurone loss by 20% or greater in response to nerve
CC
     avulsion, and effects motoneurone rescue, preferably adult motoneurone
CC
     rescue. The MGF polynucleotide and polypeptide are useful in the
CC
    manufacture of a medicament for the treatment of a neurological disorder,
CC
     including a disorder of motoneurones and/or neurodegenerative disorder,
```

```
CC
    e.g., amyotrophic lateral sclerosis, spinal muscular atrophy, progressive
CC
    spinal muscular atrophy, infantile or juvenile muscular atrophy,
CC
    poliomyelitis or post-polio syndrome, a disorder caused by exposure to a
    toxin, motoneurone trauma, a motoneurone lesion or nerve damage, an
CC
    injury that affects motoneurones, motoneurone loss associated with aging,
CC
CC
    autosomal or sex-linked muscular dystrophy, diabetic neuropathy,
CC
    peripheral neuropathies, Alzheimer's disease and Parkinson's disease.
    The present sequence is rabbit IGF-I isoform MGF cDNA. MGF is a muscle
CC
CC
    isoform having extracellular (Ec) domain, hence also referred as
    IGF-I-Ec. The MGF protein comprises amino acid sequences encoded by
CC
CC
    nucleic acid sequence of IGF-I exons 4, 5 and 6 in the reading frame
    of MGF.
CC
XX
    Sequence 523 BP; 154 A; 129 C; 142 G; 98 T; 0 other;
SO
 Query Match
                    100.0%; Score 523; DB 22;
                                          Length 523;
 Best Local Similarity
                    100.0%; Pred. No. 5.1e-144;
 Matches 523; Conservative
                         0: Mismatches
                                       0: Indels
                                                           0;
                                                     Gaps
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           1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
Dh
        61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
Qу
           Db
        61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
       121 ACAGGCATCGTGGATGATGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
Qу
           Db
       121 ACAGGCATCGTGGATGATGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
       Qу
          Db
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Qу
           241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
Db
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Qу
          301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
Db
       361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
Qу
           361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
Db
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Qу
           Db
       421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
       481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
Qу
           Db
       481 CAAAGATGGCATTTCCCCCCAATGAAATACACAAGTAAACATTC 523
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     AAS16879 standard; cDNA; 523 BP.
XX
AC
     AAS16879;
XX
DT
     25-FEB-2002 (first entry)
XX
DE
     Rabbit mechano-growth factor (MGF) cDNA.
XX
KW
     Rabbit; mechano-growth factor; insulin-like growth factor I; IGF-I; MGF;
KW
     neuroprotective; nerve damage; peripheral nervous system; nerve severing;
     muscle; neurological disorder; motoneuron loss; motorneuron disorder; ss;
KW
     nerve avulsion.
KW
XX
OS
     Oryctolagus cuniculus.
XX
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                     1..336
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                     /product= "Rabbit MGF"
FT
FT
                     /partial
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                     /note= "No start codon"
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FT
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FT
FT
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FT
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FT
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FT
                     311..333
FT
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FT
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FT
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PN
     WO200185781-A2.
XX
PD
     15-NOV-2001.
XX
PF
     10-MAY-2001; 2001WO-GB02054.
XX
     10-MAY-2000; 2000GB-0011278.
PR
XX
PΑ
     (UNLO ) UNIV COLLEGE LONDON.
PΑ
     (EGRI-) EAST GRINSTEAD MEDICAL RES TRUST.
XX
PΙ
     Goldspink G, Terenghi G;
XX
DR
     WPI; 2002-055585/07.
     P-PSDB; AAU10561.
DR
XX
PT
     Use of insulin-like growth factor I (IGF-I) isoform known as
     mechano-growth factor which is encoded by IGF-I exons 4,5,6 and has
PT
PT
     ability to reduce motoneuron loss in response to nerve avulsion, to
PT
     treat nerve damage -
XX
PS
     Disclosure; Fig 7; 65pp; English.
```

```
XX
CC
    The invention relates to the use of an insulin-like growth factor I
CC
    (IGF-I) isoform, known as mechano-growth factor (MGF), in the manufacture
CC
    of a medicament for treating nerve damage in the peripheral nervous
CC
    system, or for treating nerve damage by localising MGF at the site of
CC
    damage. The nerve damage may include severing of a nerve. The treatment
CC
    may be combined with another treatment (such as a polypeptide growth
    factor other than MGF) that prevents or diminishes degeneration of the
CC
    target organ (for example, muscle) which the damaged nerve innervates,
CC
   whereby the treatment of the muscle with MGF or a polynucleotide encoding
CC
CC
    MGF prevents or diminishes degeneration. The method is useful for
CC
    treating neurological disorders, preferably motorneuron disorders. These
    methods can reduce motoneuron loss by 20% or greater in response to nerve
CC
CC
    avulsion. This sequence represents cDNA encoding the rabbit MGF.
XX
SO
    Sequence 523 BP; 154 A; 129 C; 142 G; 98 T; 0 other;
 Query Match
                    100.0%; Score 523; DB 24; Length 523;
 Best Local Similarity 100.0%; Pred. No. 5.1e-144;
 Matches 523; Conservative
                         0: Mismatches
                                        0; Indels
                                                      Gaps
                                                            0;
         1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGGAGAC 60
Qy
           Db
         1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
Qy
        61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
           61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
Db
       121 ACAGGCATCGTGGATGATGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
Qy
           121 ACAGGCATCGTGGATGATGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
Db
       Qy
           Db
       241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
Qу
           241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
Db
       301 AGAAGGAAAGGAAGTACATTTGAAGAACACÁAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
Qy
           301 AGAAGGAAAGGAAGTACATTTGAAGAACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
Db
       361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
Qγ
           361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
Db
       421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
Qy
           421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
Db
Qу
       481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
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481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523

Db

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RESULT 3
AAT84893
ΙD
     AAT84893 standard; cDNA; 553 BP.
XX
AC
     AAT84893;
XX
DT
     14-APR-1998 (first entry)
XX
     Rabbit insulin like growth factor 1 encoding cDNA.
DΕ
XX
KW
     Insulin like growth factor 1; IGF-1; Ec peptide; muscle disorder;
KW
     heart; neuromuscular disease; primer; ss.
XX
OS
     Oryctolagus cuniculus.
XX
                     Location/Qualifiers
FH
\mathbf{FT}
     CDS
                     1..366
FT
                     /*tag= a
FT
                     /product= "IGF-1"
XX
PN
     WO9733997-A1.
XX
PD
     18-SEP-1997.
XX
PF
     11-MAR-1997;
                    97WO-GB00658.
XX
PR
     11-MAR-1996;
                    96GB-0005124.
XX
     (UNLO ) ROYAL FREE HOSPITAL SCHOOL MED.
PA
XX
PΙ
     Goldspink G;
XX
DR
     WPI; 1997-470877/43.
DR
     P-PSDB; AAW23301.
XX
PT
     Use of insulin like growth factor I characterised by presence of Ec
     peptide - to treat humans or animals, particularly muscle disorders,
PТ
PT
     heart conditions or neuromuscular diseases
XX
PS
     Disclosure; Fig 3; 33pp; English.
XX
     A use of insulin like growth factor I (IGF-1) has been developed, and
CC
CC
     is characterised by the presence of the Ec peptide, or a functional
CC
     equivalent, in the treatment or therapy of a human or animal. The IGF-1
CC
     polypeptide can be used to treat muscular disorders, e.g. Duchenne or
CC
     Becker muscular dystrophy, autosomal dystrophies and related progressive
CC
     skeletal muscle weakness and wasting, muscle atrophy in ageing humans,
CC
     spinal cord injury induced muscle atrophy and neuromuscular diseases,
CC
     and cardiac disorders, e.g. diseases where promotion of cardiac muscle
CC
     protein synthesis is a beneficial treatment, cardiomyopathies and acute
CC
     heart failure or insult, specifically myocarditis or myocardial
CC
     infarction. It can also be used to promote bone fracture healing and
CC
     maintenance of bone in old age. The present sequence encodes rabbit
CC
     IGF-1 used in the present specification.
XX
SQ
     Sequence 553 BP; 159 A; 142 C; 147 G; 105 T; 0 other;
```

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Query Match
                   100.0%; Score 523; DB 18;
                                        Length 553;
 Best Local Similarity
                   100.0%; Pred. No. 5.3e-144;
 Matches 523; Conservative
                        0; Mismatches
                                     0; Indels
                                                0;
                                                  Gaps
                                                         0;
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Qу
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Db
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Qу
          91 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 150
Db
       121 ACAGGCATCGTGGATGATGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
Qу
          151 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 210
Db
       Qy
          Db
       241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAATGAAGTCTCAGAGG 300
Qу
          Db
       271 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 330
Qy
       301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGGAGTGCAGGAAACAAGAACTA 360
          Db
       331 AGAAGGAAAGGAAGTACATTTGAAGAACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 390
Qу
       361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
          391 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 450
Db
Qy
       421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
          Db
       451 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 510
       481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
Qу
          511 CAAAGATGGCATTTCCCCCCAATGAAATACACAAGTAAACATTC 553
Db
RESULT 4
   AAD06398 standard; cDNA; 517 BP.
XX
AC
   AAD06398;
XX
DT
   10-AUG-2001
            (first entry)
XX
DE
   Human IGF-I isoform mechano-growth factor (MGF) cDNA.
XX
KW
   Human; IGF-I isoform; Insulin-like Growth Factor-I; MGF;
KW
   mechano-growth factor; neurological disorder; neurodegenerative disorder;
KW
   amyotrophic lateral sclerosis; spinal muscular atrophy; muscular atrophy;
KW
   poliomyelitis; post-polio syndrome; toxin; motoneurone disorder;
KW
   nerve damage; autosomal muscular dystrophy; diabetic neuropathy;
```

```
ΚW
     sex-linked muscular dystrophy; peripheral neuropathy;
KW
     Alzheimer's disease; Parkinson's disease; ss.
XX
OS
     Homo sapiens.
XX
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                     Location/Qualifiers
     Key
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     CDS
                     1..333
FT
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                     /product= "Mechano-growth factor (MGF)"
                     /note= "This region comprises exons 3-6. The CDS does
FT
FT
                     not include start codon"
FT
                     /partial
XX
     WO200136483-A1.
ΡN
XX
PD
     25-MAY-2001.
XX
     15-NOV-2000; 2000WO-GB04354.
PF
XX
PR
     15-NOV-1999;
                    99GB-0026968.
XX
     (UNLO ) UNIV COLLEGE LONDON.
PA
XX
PΙ
     Goldspink G, Johnson I;
XX
DR
     WPI; 2001-355620/37.
DR
     P-PSDB; AAE02447.
XX
     Use of mechano-growth factor, an isoform of Insulin-like Growth
PT
PT
     Factor-I, capable of reducing motoneurone loss, in the manufacture of a
PТ
     medicament for the treatment of neurological disorder -
XX
PS
     Claim 4; Page 49-50; 66pp; English.
XX
CC
     The present invention relates to use of mechano-growth factor (MGF),
     an Insulin-like Growth Factor-I (IGF-I) isoform in the manufacture of a
CC
CC
    medicament for the treatment of neurological disorder. The MGF is capable
CC
     of reducing motoneurone loss by 20% or greater in response to nerve
CC
     avulsion, and effects motoneurone rescue, preferably adult motoneurone
CC
     rescue. The MGF polynucleotide and polypeptide are useful in the
CC
    manufacture of a medicament for the treatment of a neurological disorder,
CC
     including a disorder of motoneurones and/or neurodegenerative disorder,
CC
     e.g., amyotrophic lateral sclerosis, spinal muscular atrophy, progressive
CC
     spinal muscular atrophy, infantile or juvenile muscular atrophy,
     poliomyelitis or post-polio syndrome, a disorder caused by exposure to a
CC
CC
     toxin, motoneurone trauma, a motoneurone lesion or nerve damage, an
CC
     injury that affects motoneurones, motoneurone loss associated with aging,
CC
     autosomal or sex-linked muscular dystrophy, diabetic neuropathy,
CC
     peripheral neuropathies, Alzheimer's disease and Parkinson's disease.
CC
     The present sequence is human IGF-I isoform MGF cDNA. MGF is a muscle
CC
     isoform having extracellular (Ec) domain, hence also referred as
CC
     IGF-I-Ec. The MGF protein comprises amino acid sequences encoded by
CC
     nucleic acid sequence of IGF-I exons 4, 5 and 6 in the reading frame
CC
     of MGF.
XX
SO
     Sequence 517 BP; 150 A; 130 C; 139 G; 98 T; 0 other;
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Query Match
                   89.4%; Score 467.4; DB 22; Length 517;
 Best Local Similarity
                   96.2%;
                         Pred. No. 1.3e-127;
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                         0: Mismatches
                                      16: Indels
                                                    Gaps
                                                          2:
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          Db
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          121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
Db
       Qу
          Db
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Qу
          Db
       241 ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCA---G 297
Qy
       301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
          Db
       298 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 357
Qу
       361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
          Db
       358 CAGGATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 416
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Qу
          Db
       417 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 476
       481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACAT 521
Qу
          477 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACAT 517
Db
RESULT 5
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   AAS16877 standard; cDNA; 517 BP.
XX
AC
   AAS16877;
XX
DT
   25-FEB-2002
             (first entry)
XX
DE
   Human mechano-growth factor (MGF) cDNA.
XX
KW
   Human; mechano-growth factor; insulin-like growth factor I; IGF-I; MGF;
ΚW
   neuroprotective; nerve damage; peripheral nervous system; nerve severing;
KW
   muscle; neurological disorder; motoneuron loss; motorneuron disorder; ss;
KW
   nerve avulsion.
XX
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OS

Homo sapiens.

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XX
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     15-NOV-2001.
XX
PF
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XX
PR
     10-MAY-2000; 2000GB-0011278.
XX
PA
     (UNLO ) UNIV COLLEGE LONDON.
     (EGRI-) EAST GRINSTEAD MEDICAL RES TRUST.
PA
XX
PΙ
     Goldspink G, Terenghi G;
XX
DR
     WPI; 2002-055585/07.
DR
     P-PSDB; AAU10559.
XX
PT
     Use of insulin-like growth factor I (IGF-I) isoform known as
PT
     mechano-growth factor which is encoded by IGF-I exons 4,5,6 and has
PT
     ability to reduce motoneuron loss in response to nerve avulsion, to
PT
     treat nerve damage -
XX
PS
     Claim 11; Fig 5; 65pp; English.
XX
CC
     The invention relates to the use of an insulin-like growth factor I
CC
     (IGF-I) isoform, known as mechano-growth factor (MGF), in the manufacture
CC
     of a medicament for treating nerve damage in the peripheral nervous
CC
     system, or for treating nerve damage by localising MGF at the site of
CC
     damage. The nerve damage may include severing of a nerve. The treatment
CC
     may be combined with another treatment (such as a polypeptide growth
CC
     factor other than MGF) that prevents or diminishes degeneration of the
CC
     target organ (for example, muscle) which the damaged nerve innervates,
CC
     whereby the treatment of the muscle with MGF or a polynucleotide encoding
CC
     MGF prevents or diminishes degeneration. The method is useful for
CC
     treating neurological disorders, preferably motorneuron disorders. These
CC
     methods can reduce motoneuron loss by 20% or greater in response to nerve
CC
     avulsion. This sequence represents cDNA encoding the human MGF.
```

(

XX

```
Query Match
                   89.4%; Score 467.4; DB 24; Length 517;
 Best Local Similarity 96.2%; Pred. No. 1.3e-127;
 Matches 501; Conservative
                         0; Mismatches
                                      16:
                                         Indels
                                                    Gaps
                                                          2;
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Qу
          1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGGAGAC 60
Db
        61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
Qу
          61 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
Db
       121 ACAGGCATCGTGGATGATGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
Qу
          121 ACAGGCATCGTGGATGATGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
Db
       Qу
          181 TGCGCACCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 240
Db
       241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
Qу
          Db
       241 ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCA---G 297
Qу
       301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
          298 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 357
Db
       361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
Qy
          358 CAGGATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 416
Db
       421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
Qy
          Db
       417 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 476
       481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACAT 521
Qy
          477 CAAAGATGGCATTTCCCCCCAATGAAATACACAAGTAAACAT 517
Db
RESULT 6
AAD06405
   AAD06405 standard; cDNA; 471 BP.
ID
XX
   AAD06405;
AC
XX
DT
   10-AUG-2001 (first entry)
XX
DE
   Rabbit liver-type IGF-I isoform (L.IGF-I) cDNA.
XX
KW
   Rabbit; IGF-I isoform; Insulin-like Growth Factor-I; MGF;
KW
   mechano-growth factor; neurological disorder; neurodegenerative disorder;
KW
   amyotrophic lateral sclerosis; spinal muscular atrophy; muscular atrophy;
KW
   poliomyelitis; post-polio syndrome; toxin; motoneurone disorder;
```

```
KW
     nerve damage; autosomal muscular dystrophy; diabetic neuropathy;
     sex-linked muscular dystrophy; peripheral neuropathy;
KW
KW
     Alzheimer's disease; Parkinson's disease; liver; L.IGF-I; ss.
XX
OS
     Oryctolagus cuniculus.
XX
FΗ
     Key
                     Location/Qualifiers
FT
     CDS
                     1..318
FT
                     /*tag= a
FT
                     /product= "Liver-type IGF-I isoform (L.IGF-I)"
FT
                     /transl except= (pos:7..9, aa:Gln)
FT
                     /transl except= (pos:25..27, aa:Gln)
                     /note= "These translation exceptions occur while decoding
FT
FT
                     the alternative version of the protein (AAE02456).
FT
                     The CDS comprises exons 3, 4 and 6 and
                     does not include start codon"
FT
                     /partial
FT
XX
ΡN
     WO200136483-A1.
XX
     25-MAY-2001.
PD
XX
PF
     15-NOV-2000; 2000WO-GB04354.
XX
PR
     15-NOV-1999;
                    99GB-0026968.
XX
PA
     (UNLO ) UNIV COLLEGE LONDON.
XX
PΙ
     Goldspink G, Johnson I;
XX
DR
     WPI; 2001-355620/37.
DR
     P-PSDB; AAE02452, AAE02456.
XX
     Use of mechano-growth factor, an isoform of Insulin-like Growth
PT
PT
     Factor-I, capable of reducing motoneurone loss, in the manufacture of a
PT
     medicament for the treatment of neurological disorder -
XX
PS
     Disclosure; Page 59-60; 66pp; English.
XX
CC
     The present invention relates to use of mechano-growth factor (MGF),
CC
     an Insulin-like Growth Factor-I (IGF-I) isoform in the manufacture of a
CC
     medicament for the treatment of neurological disorder. The MGF is capable
CC
     of reducing motoneurone loss by 20% or greater in response to nerve
CC
     avulsion, and effects motoneurone rescue, preferably adult motoneurone
CC
     rescue. The MGF polynucleotide and polypeptide are useful in the
CC
     manufacture of a medicament for the treatment of a neurological disorder,
CC
     including a disorder of motoneurones and/or neurodegenerative disorder,
CC
     e.g., amyotrophic lateral sclerosis, spinal muscular atrophy, progressive
CC
     spinal muscular atrophy, infantile or juvenile muscular atrophy,
CC
     poliomyelitis or post-polio syndrome, a disorder caused by exposure to a
CC
     toxin, motoneurone trauma, a motoneurone lesion or nerve damage, an
CC
     injury that affects motoneurones, motoneurone loss associated with aging,
CC
     autosomal or sex-linked muscular dystrophy, diabetic neuropathy,
CC
     peripheral neuropathies, Alzheimer's disease and Parkinson's disease.
CC
     The present sequence is rabbit liver-type IGF-I isoform (L.IGF-I) cDNA.
CC
     The L.IGF-I protein comprises amino acid sequences encoded by
CC
     nucleic acid sequence of IGF-I exons 4 and 6.
```

```
XX
SO
```

Sequence 471 BP; 132 A; 118 C; 131 G; 90 T; 0 other;

```
Query Match
                  78.2%; Score 409; DB 22; Length 471;
 Best Local Similarity 90.1%; Pred. No. 2e-110;
 Matches 471; Conservative
                       0; Mismatches
                                  0; Indels
                                                       1;
        1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
Qу
          Db
        1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
        61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
Qу
          61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
Db
       121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
Qу
          121 ACAGGCATCGTGGATGATGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
Db
       Qу
          Db
       241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAATGAAGTCTCAGAGG 300
Qу
          Db
       241 ATGCCCAAGACTCAG----- 255
Qу
       301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
               256 -----AAGGAAGTACATTTGAAGAACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 308
Db
       361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
Qу
          309 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 368
Db
       421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
Qу
          369 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 428
Db
       481 CAAAGATGGCATTTCCCCCCAATGAAATACACAAGTAAACATTC 523
Qу
          Dh
       429 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 471
RESULT 7
   AAS16884 standard; cDNA; 471 BP.
XX
AC
   AAS16884;
XX
DT
   25-FEB-2002 (first entry)
XX
DE
   Rabbit insulin-like growth factor I liver-type isoform (L.IGF-I) cDNA.
XX
KW
   Rabbit; mechano-growth factor; insulin-like growth factor I; IGF-I; MGF;
KW
   neuroprotective; nerve damage; peripheral nervous system; nerve severing;
ΚW
   muscle; neurological disorder; motoneuron loss; motorneuron disorder; ss;
```

```
KW
     nerve avulsion; insulin-like growth factor I liver-type isoform; L.IGF-I;
XX
OS
     Oryctolagus cuniculus.
XX
FH
     Key
                     Location/Qualifiers
FT
     CDS
                     1..318
FΤ
                     /*tag=
FΤ
                     /product= "Rabbit L.IGF-I"
FT
                     /partial
FT
                     /note= "No start codon"
FT
                     1..75
     exon
FT
                     /*tag= b
                     /number= exon 3
FT
FT
                     76..258
     exon
FT
                     /*tag= c
FT
                     /number= exon 4
                     259..315
FT
     exon
FT
                     /*tag= d
FT
                     /number= exon 6
XX
PN
     WO200185781-A2.
XX
ΡĎ
     15-NOV-2001.
XX
PF
     10-MAY-2001; 2001WO-GB02054.
XX
PR
     10-MAY-2000; 2000GB-0011278.
XX
PA
     (UNLO ) UNIV COLLEGE LONDON.
     (EGRI-) EAST GRINSTEAD MEDICAL RES TRUST.
PΑ
XX
PΙ
     Goldspink G, Terenghi G;
XX
DR
     WPI; 2002-055585/07.
DR
     P-PSDB; AAU10564.
XX
PT
     Use of insulin-like growth factor I (IGF-I) isoform known as
PT
     mechano-growth factor which is encoded by IGF-I exons 4,5,6 and has
PT
     ability to reduce motoneuron loss in response to nerve avulsion, to
PT
     treat nerve damage -
XX
PS
     Disclosure; Fig 10; 65pp; English.
XX
CC
     The invention relates to the use of an insulin-like growth factor I
CC
     (IGF-I) isoform, known as mechano-growth factor (MGF), in the manufacture
CC
     of a medicament for treating nerve damage in the peripheral nervous
CC
     system, or for treating nerve damage by localising MGF at the site of
CC
     damage. The nerve damage may include severing of a nerve. The treatment
    may be combined with another treatment (such as a polypeptide growth
CC
CC
     factor other than MGF) that prevents or diminishes degeneration of the
CC
     target organ (for example, muscle) which the damaged nerve innervates,
CC
     whereby the treatment of the muscle with MGF or a polynucleotide encoding
CC
    MGF prevents or diminishes degeneration. The method is useful for
     treating neurological disorders, preferably motorneuron disorders. These
CC
CC
     methods can reduce motoneuron loss by 20% or greater in response to nerve
CC
     avulsion. This sequence represents cDNA encoding the rabbit insulin-like
CC
     growth factor I liver-type isoform (L.IGF-I) used in experiments on
```

```
CC
   motoneuron loss.
XX
SQ
   Sequence 471 BP; 132 A; 118 C; 131 G; 90 T; 0 other;
 Query Match
                   78.2%; Score 409; DB 24; Length 471;
 Best Local Similarity
                   90.1%; Pred. No. 2e-110;
       471; Conservative
                        0; Mismatches
                                     0;
                                       Indels
                                              52:
                                                  Gaps
                                                        1:
        1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
Qу
          Db
        1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
        61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
Qy
          Db
        61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
       121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
Qу
          Db
       121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
       Qy
          Db
       241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
Qy
          11111111111111
Db
       241 ATGCCCAAGACTCAG----- 255
Qу
       301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
               Db
       256 -----AAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 308
       361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
Qу
          309 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 368
Db
       421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
Qу
          369 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 428
Db
       481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
Qу
          429 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 471
Db
RESULT 8
AAD06399
   AAD06399 standard; cDNA; 539 BP.
ID
XX
   AAD06399;
AC
XX
DT
   10-AUG-2001 (first entry)
XX
DE
   Rat IGF-I isoform mechano-growth factor (MGF) cDNA.
XX
KW
   Rat; IGF-I isoform; Insulin-like Growth Factor-I; MGF;
   mechano-growth factor; neurological disorder; neurodegenerative disorder;
KW
```

```
KW
     amyotrophic lateral sclerosis; spinal muscular atrophy; muscular atrophy;
KW
     poliomyelitis; post-polio syndrome; toxin; motoneurone disorder;
KW
     nerve damage; autosomal muscular dystrophy; diabetic neuropathy;
     sex-linked muscular dystrophy; peripheral neuropathy;
KW
KW
     Alzheimer's disease; Parkinson's disease; ss.
XX
OS
     Rattus sp.
XX
FΗ
     Key
                     Location/Qualifiers
FT
     CDS
                     1..336
FT
                     /*taq=a
FT
                     /product= "Mechano-growth factor (MGF)"
                     /note= "This region comprises exons 3-6. The CDS does
FT
FT
                     not include start codon"
FT
                     /partial
XX
PN
     WO200136483-A1.
XX
PD
     25-MAY-2001.
XX
     15-NOV-2000; 2000WO-GB04354.
PF
XX
PR
     15-NOV-1999;
                    99GB-0026968.
XX
PA
     (UNLO ) UNIV COLLEGE LONDON.
XX
     Goldspink G, Johnson I;
PI
XX
     WPI: 2001-355620/37.
DR
     P-PSDB; AAE02448.
DR
XX
     Use of mechano-growth factor, an isoform of Insulin-like Growth
PT
     Factor-I, capable of reducing motoneurone loss, in the manufacture of a
PT
PT
     medicament for the treatment of neurological disorder -
XX
PS
     Claim 4; Page 51-52; 66pp; English.
XX
CC
     The present invention relates to use of mechano-growth factor (MGF),
CC
     an Insulin-like Growth Factor-I (IGF-I) isoform in the manufacture of a
     medicament for the treatment of neurological disorder. The MGF is capable
CC
CC
     of reducing motoneurone loss by 20% or greater in response to nerve
CC
     avulsion, and effects motoneurone rescue, preferably adult motoneurone
CC
     rescue. The MGF polynucleotide and polypeptide are useful in the
CC
     manufacture of a medicament for the treatment of a neurological disorder,
     including a disorder of motoneurones and/or neurodegenerative disorder,
CC
CC
     e.g., amyotrophic lateral sclerosis, spinal muscular atrophy, progressive
CC
     spinal muscular atrophy, infantile or juvenile muscular atrophy,
CC
     poliomyelitis or post-polio syndrome, a disorder caused by exposure to a
CC
     toxin, motoneurone trauma, a motoneurone lesion or nerve damage, an
CC
     injury that affects motoneurones, motoneurone loss associated with aging,
CC
     autosomal or sex-linked muscular dystrophy, diabetic neuropathy,
CC
     peripheral neuropathies, Alzheimer's disease and Parkinson's disease.
     The present sequence is rat IGF-I isoform MGF cDNA. MGF is a muscle
CC
CC
     isoform having extracellular (Ec) domain, hence also referred as
CC
     IGF-I-Ec. The MGF protein comprises amino acid sequences encoded by
CC
     nucleic acid sequence of IGF-I exons 4, 5 and 6 in the reading frame
```

CC

of MGF.

```
XX
SO
```

Sequence 539 BP; 161 A; 136 C; 139 G; 103 T; 0 other;

```
Query Match
                    68.2%; Score 356.8; DB 22; Length 539;
 Best Local Similarity
                    82.3%; Pred. No. 5.1e-95;
 Matches 436; Conservative
                         0; Mismatches 87; Indels
                                                           2;
         1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
Qу
           Db
         1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGGACCA 60
        61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
Qy
           61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
Db
       121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
Qу
           121 ACGGGCATTGTGGATGATGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
Db
       Qу
           Db
       181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
       241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
Qу
           Db
       241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
Qу
       301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
           301 AGAAGGAAAGGAAGTACACTTGAAGAACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
Db
       361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
Qу
           361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
Db
       421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA----AAAAATAAGTTTGATC 474
Qу
          \prod
                    1
                        141111 1111 111 1111
                                            421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480
Db
       475 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
Qу
           481 TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTC 530
Db
RESULT 9
   AAS16878 standard; cDNA; 539 BP.
XX
AC
   AAS16878;
XX
DT
   25-FEB-2002 (first entry)
XX
DΕ
   Rat mechano-growth factor (MGF) cDNA.
XX
KW
    Rat; mechano-growth factor; insulin-like growth factor I; IGF-I; MGF;
KW
    neuroprotective; nerve damage; peripheral nervous system; nerve severing;
   muscle; neurological disorder; motoneuron loss; motorneuron disorder; ss;
KW
```

```
KW
     nerve avulsion.
XX
OS
     Rattus sp.
XX
FH
                     Location/Qualifiers
     Key
FT
     CDS
                     1..336
FT
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FT
                     /product= "Rat MGF"
FT
                     /partial
FT
                     /note= "No start codon"
FT
                     1..75
     exon
FT
                     /*tag= b
                     /number= exon 3
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FT
                     /number= exon 4
                     259..309
FT
     exon
FT
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FT
                     310..333
     exon
FT
                     /*tag= e
                     /number= exon 6
FT
XX
    WO200185781-A2.
PN
XX
PD
     15-NOV-2001.
XX
    10-MAY-2001; 2001WO-GB02054.
PF
XX
PR
     10-MAY-2000; 2000GB-0011278.
XX
PΑ
     (UNLO ) UNIV COLLEGE LONDON.
PA
     (EGRI-) EAST GRINSTEAD MEDICAL RES TRUST.
XX
PI
     Goldspink G, Terenghi G;
XX
DR
     WPI; 2002-055585/07.
DR
     P-PSDB; AAU10560.
XX
PT
     Use of insulin-like growth factor I (IGF-I) isoform known as
     mechano-growth factor which is encoded by IGF-I exons 4,5,6 and has
PT
     ability to reduce motoneuron loss in response to nerve avulsion, to
PT
     treat nerve damage
PT
XX
PS
     Disclosure; Fig 6; 65pp; English.
XX
CC
     The invention relates to the use of an insulin-like growth factor I
CC
     (IGF-I) isoform, known as mechano-growth factor (MGF), in the manufacture
CC
     of a medicament for treating nerve damage in the peripheral nervous
     system, or for treating nerve damage by localising MGF at the site of
CC
CC
     damage. The nerve damage may include severing of a nerve. The treatment
CC
     may be combined with another treatment (such as a polypeptide growth
CC
     factor other than MGF) that prevents or diminishes degeneration of the
CC
     target organ (for example, muscle) which the damaged nerve innervates,
CC
     whereby the treatment of the muscle with MGF or a polynucleotide encoding
CC
     MGF prevents or diminishes degeneration. The method is useful for
CC
     treating neurological disorders, preferably motorneuron disorders. These
```

```
CC
    methods can reduce motoneuron loss by 20% or greater in response to nerve
CC
    avulsion. This sequence represents cDNA encoding the rat MGF.
XX
SO
    Sequence 539 BP; 161 A; 136 C; 139 G; 103 T; 0 other;
                    68.2%; Score 356.8; DB 24; Length 539;
 Best Local Similarity
                    82.3%; Pred. No. 5.1e-95;
 Matches 436; Conservative
                         0; Mismatches 87; Indels
                                                           2;
                                                 7; Gaps
         1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGGAGAC 60
Qy
           Db
         1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60
        61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
Qy
          Db
        61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
       121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
Qy
           Db
       121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
       Qy
          Db
       181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
Qу
       241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
          241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
Db
       301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
Qу
          301 AGAAGGAAAGGAAGTACACTTGAAGAACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
Db
       361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
Qy
          361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
Db
       421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA-----AAAAATAAGTTTGATC 474
Qу
          \Pi
                    1
                        421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480
Db
       475 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
Qу
           481 TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTC 530
Db
RESULT 10
ABV76185
ID
   ABV76185 standard; cDNA; 651 BP.
XX
AC
   ABV76185;
XX
   07-MAR-2003 (first entry)
DT
XX
DE
   Mouse insulin-like growth factor IB cDNA.
XX
KW
   Insulin-like growth factor IB; IGF-IB; mouse; mRNA; assay;
```

```
KW
     nucleic acid detection; gene; ss.
XX
OS
     Mus musculus.
XX
FH
     Key
                     Location/Qualifiers
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     CDS
                     73..474
FT
                     /*tag= a
FT
                     /product= "IGF-IB"
XX
ΡN
     WO200297390-A2.
XX
     05-DEC-2002.
PD
XX
PF
     31-MAY-2002; 2002WO-SE01056.
XX
     01-JUN-2001; 2001SE-0001934.
PR
XX
PΑ
     (BIOV-) BIOVITRUM AB.
XX
PI
     Parrow V, Rosengren L;
XX
DR
     WPI; 2003-129529/12.
XX
PT
     Quantitating a target nucleic acid in a sample comprises immobilizing,
РΤ
     on a solid support, a sample comprising a target nucleic acid, and
PT
     detecting and quantitating signals generated from the antisense and
PT
     sense probes -
XX
PS
     Example 1; Page 16-17; 18pp; English.
XX
CC
     The present sequence is that of cDNA encoding murine insulin-like
CC
     growth factor 1B (IGF-IB). The cDNA was used in an example of the
CC
     method of the invention to generate probes for determination of
CC
     IGF-IB RNA. The method comprises a quantitative hybridisation
CC
     assay for analysis of mRNA in a target nucleic acid (TNA) sample.
CC
     It involves: (i) immobilising the TNA sample on a solid support;
CC
     (ii) contacting a labelled antisense probe to a first portion of the
CC
     TNA, and a labelled sense probe to a second portion of the TNA;
CC
     (iii) detecting and quantitating the signals generated from the
CC
     hybridised probes; and (iv) determining the value represented by
CC
     the antisense probe signal minus the sense probe signal, the value
CC
     being proportional to the amount of mRNA in the TNA sample. In an
CC
     example of the method, a cDNA clone containing 60 nucleotides from
CC
     exon 2 and 179 nucleotides from exon 3 of the mouse IGF-IB gene was
CC
     cloned into pGEN-4Z vector. Linearisation of the plasmid with
CC
     EcoRI allowed transcription of a 250-nucleotide antisense probe
CC
     using T7 polymerase. Linearisation with HindIII allowed
CC
     transcription of a sense probe of similar length using SP6
CC
     polymerase (see ABV76186). The probes were purified and used to
CC
     determine IGF-I RNA in mouse hepatocytes and also in rat hepatocytes.
XX
SO
     Sequence 651 BP; 193 A; 185 C; 149 G; 124 T; 0 other;
  Query Match
                          66.8%; Score 349.4; DB 25; Length 651;
```

82.8%; Pred. No. 8.3e-93;

0; Mismatches

81; Indels

Best Local Similarity

Matches 425; Conservative

```
Qу
        1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
          Db
       139 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGGACCG 198
        61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
Qу
          199 AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCTCAG 258
Db
Qу
       121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
          259 ACAGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGACTGGAGATGTAC 318
Db
       Qу
          319 TGTGCCCCACTGAAGCCTACAAAAGCAGCCCGCTCTATCCGTGCCCAGCGCCACACTGAC 378
Db
       241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
Qу
          11 111
       Db
Qy
       301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
          439 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 498
Db
       361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
Qy
          Db
       499 CAGAATGTAGGAGGAGCCTCCCACGGAGCAGAAAATGCCACATCACCGCAGGATCCTTTG 558
       421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA----AAAAATAAGTTTGATC 474
Qу
          11
                       11 111111
       559 CTGCTTGAGCAACCTGCAAAACATCGAAACACCTACCAAATAACAATAATAAGTCCAATA 618
Db
Qу
       475 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAA 506
          619 ACATTACAAAGATGGGCATTTCCCCCAATGAAA 651
Db
RESULT 11
AAN70436
   AAN70436 standard; cDNA; 818 BP.
ID
XX
AC
   AAN70436;
XX
   25-MAR-2003
DT
             (updated)
DT
   05-APR-1991
             (first entry)
XX
DE
   Sequence encoding insulin-like growth factor 1A (IGF-1A).
XX
KW
   Growth promoter; lactation enhancer; cell proliferation; ss.
XX
OS
   Homo sapiens.
XX
PN
   EP229750-A.
XX
PD
   22-JUL-1987.
XX
PF
              87EP-0870001.
   06-JAN-1987;
```

```
XX
PR
    20-NOV-1986;
                86US-0929671.
PR
    07-JAN-1986;
                 86US-0816662.
XX
PA
    (UNIW ) UNIV WASHINGTON.
XX
PΙ
    Krivi GG, Rotwein PS;
XX
DR
    WPI; 1987-200203/29.
XX
PT
    New pre-pro-insulin-like growth factor-1 protein - obtd. by
PT
    recombinant DNA procedures for use as growth promoters for
PT
    enhancing lactation, for stimulating cell proliferation etc.
XX
PS
    Example; Fig 5; 59pp; English.
XX
CC
    A 42 base oligonucleotide corresponding to the DNA sequence encoding
CC
    amino acids 10 to 23 of mature human IGF-I was synthesized (AAN70437).
CC
    The radiolabeled 42 mer was then employed to screen for IGF-I
CC
    containing DNA sequences in a human liver cDNA library. Insulin-
CC
    like growth factors-1A and -1B cDNAs were isolated from a human cDNA
CC
    library by using lambdagt 11 (AAN70435, AAN70436). The human IGF-1
CC
    genomic gene was isolated and mapped. It encodes at least two
CC
    preproinsulin-like growth factor-1 proteins. An essentially pure
CC
    proproinsulin-like growth factor-1 protein comprising the sequence
CC
    of amino acids shown in Figure six is claimed (AAP70277).
CC
    (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ
    Sequence 818 BP; 232 A; 186 C; 187 G; 213 T; 0 other;
 Query Match
                     63.9%; Score 334.4; DB 8; Length 818;
 Best Local Similarity
                     84.6%; Pred. No. 2.4e-88;
 Matches 445; Conservative
                           0; Mismatches
                                         26; Indels
                                                     55;
                                                         Gaps
                                                                4;
Qу
          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
           Db
        203 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 262
         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCCACCTCAG 120
Qy
            Db
        263 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 322
        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
Qу
           Db
        323 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 382
        Qy
           383 TGCGCACCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 442
Db
        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
Qy
           Db
        443 ATGCCCAAGACCCAG----- 457
Qу
        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
                 Db
        458 -----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 510
```

```
Qy
         361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
             Db
         511 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 570
Qу
         421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
             571 CTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAATAAGTTTGATAACAT 630
Db
         479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
Qу
             631 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTC 676
Db
RESULT 12
ABT11091
    ABT11091 standard; cDNA; 7260 BP.
XX
AC
    ABT11091;
XX
DT
    04-DEC-2002 (first entry)
XX
DE
    Human breast cancer associated coding sequence SEQ ID NO: 1225.
XX
KW
    Human; breast specific gene; breast cancer; differential expression;
KW
    cytostatic; gene therapy; gene; ss.
XX
    Homo sapiens.
OS
XX
PN
    WO200259271-A2.
XX
PD
    01-AUG-2002.
XX
PF
    25-JAN-2002; 2002WO-US02176.
XX
PR
    25-JAN-2001; 2001US-263757P.
    25-APR-2001; 2001US-286090P.
PR
PR
    23-MAY-2001; 2001US-292517P.
XX
    (GENE-) GENE LOGIC INC.
PΑ
XX
PΙ
    Orr MS, Nation M, Diggans JC,
                                   Zeng W;
XX
DR
    WPI; 2002-674803/72.
XX
PT
    Diagnosing breast cancer in a patient comprises detecting the level of
    gene expression in cell or tissue samples, where a differential gene
PT
PT
    expression is indicative of breast cancer -
XX
PS
    Claim 1; SEQ ID NO 1225; 260pp + Sequence Listing; English.
XX
CC
    The present invention relates to methods of diagnosing breast cancer in a
CC
    patient, which comprise detecting the level of expression in a tissue
CC
    sample of two or more genes selected from those shown in ABT09867-
CC
    ABT11112, where a differential expression of the genes indicates breast
CC
    cancer. The methods are useful in diagnosing, treating, detecting the
CC
    progression, and in monitoring treatment of breast cancer in patients.
```

```
CC
   The methods are also useful as a screening tool for agents that modulate
CC
    the onset or progression of breast cancer. The breast cancer genes may be
CC
    used as diagnostic markers for the prediction or identification of the
CC
    malignant state of breast tissue, for confirming the type and progression
    of cancer, and for drug screening and assays. The present sequence is a
CC
CC
    coding sequence of the invention.
CC
   Note: The sequence data for this patent did not form part of the printed
CC
    specification, but was obtained in electronic format directly from WIPO
    at ftp.wipo.int/pub.published pct sequences.
CC
XX
SQ
    Sequence 7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other;
                    63.9%; Score 334.4; DB 24; Length 7260;
 Query Match
 Best Local Similarity
                    84.6%; Pred. No. 5.7e-88;
 Matches 445; Conservative
                         0; Mismatches
                                      26; Indels
                                                           4;
                                                     Gaps
         1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
Qy
          Db
       311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370
        61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
Qy
           Db
       371 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430
       121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
Qу
          Db
       431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490
Qу
       491 TGCGCACCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 550
Db
       241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
Qу
          551 ATGCCCAAGACCCAG----- 565
Db
       301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
Qу
                566 -----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 618
Db
       361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
Qу
          619 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 678
Db
       421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
Qу
           679 CTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 738
Db
       479 TTCAAAGAT-GGCATTTCCCCCCAATGAAATACACAAGTAAACATTC 523
Qy
```

739 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTC 784

RESULT 13 ABK84583

ID ABK84583 standard; cDNA; 7260 BP.

Db

```
AC
     ABK84583;
XX
DT
     14-AUG-2002 (first entry)
XX
DΕ
     Human cDNA differentially expressed in granulocytic cells #1154.
XX
KW
     Human; ss; granulocytic cell; DNA chip; bacterial infection;
KW
     viral infection; parasitic infection; protozoal infection;
KW
     fungal infection; sterile inflammatory disease; psoriasis;
KW
     rheumatoid arthritis; qlomerulonephritis; asthma; thrombosis;
KW
     cardiac reperfusion injury; renal reperfusion injury; ARDS;
     adult respiratory distress syndrome; inflammatory bowel disease;
KW
KW
     Crohn's disease; ulcerative colitis; periodontal disease;
KW
     granulocyte activation; chronic inflammation; allergy.
XX
OS
     Homo sapiens.
XX
     WO200228999-A2.
PN
XX
PD
     11-APR-2002.
XX
PF
     03-OCT-2001; 2001WO-US30821.
XX
PR
     03-OCT-2000; 2000US-237189P.
XX
PA
     (GENE-) GENE LOGIC INC.
XX
PΙ
     Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;
XX
DR
    WPI; 2002-435328/46.
XX
PT
     Detecting granulocyte activation by detecting differential expression
PT
     of genes associated with granulocyte activation, which serves as
PT
     diagnostic markers that is useful for monitoring disease states and
PT
    drug toxicity
XX
PS
     Claim 1; SEQ ID No 1154; 114pp; English.
XX
CC
     The invention relates to detecting (M1) granulocyte (GC) activation
CC
     (GCA), by detecting the level of expression of gene(s) (Gs) identified by
CC
     DNA chip analysis as given in the specification, and comparing
CC
     the expression level to an expression level in an unactivated
CC
     GC, where differential expression of Gs is indicative of GCA.
CC
    Also included are modulating (M2) GA by contacting GC with an agent
     that alters the expression of at least one gene in Gs; (2) screening (M3)
CC
CC
     for an agent capable of modulating GCA or an inflammation (especially
CC
     chronic) in a tissue, an allergic response in a subject, exposure of a
CC
     subject to a pathogen or sterile inflammatory disease using the
CC
     gene expression profile; (3) detecting (M4) an inflammation (especially
CC
     chronic) in a tissue, an allergic response in a subject, exposure of a
CC
     subject to a pathogen or sterile inflammatory disease, by detecting the
CC
     level of expression in a sample of the tissue of gene(s) from Gs, where
CC
     the level of expression of the gene is indicative of inflammation;
CC
     (4) treating (M5) an inflammation (especially chronic) or in a tissue,
CC
     an allergic response in a subject, exposure of a subject to a pathogen
CC
     or sterile inflammatory disease, by contacting a tissue having
CC
     inflammation with an agent that modulates the expression of gene(s)
```

```
CC
    from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
CC
    modulating GA; M3 is useful for screening an agent capable of modulating
CC
    GCA preferably in an inflammation in a tissue; M4 is useful for
CC
    detecting an inflammation (especially chronic) in a tissue, an allergic
CC
    response in a subject, exposure of a subject to a pathogen or sterile
CC
    inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
CC
    glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
CC
    reperfusion injury, ARDS, adult respiratory distress syndrome,
CC
    inflammatory bowel disease, Crohn's disease, ulcerative colitis,
CC
    periodontal disease; also bacterial infection, viral infection,
CC
    parasitic infection, protozoal infection, fungal infection and M5 is
    useful for treating one of the above conditions. The present
CC
CC
    sequence represents a gene differentially expressed in granulocytes.
CC
    Note: The sequence data for this patent did not form part
CC
    of the printed specification, but was obtained in electronic
CC
    format directly from WIPO at
CC
    ftp.wipo.int/pub/published pct sequences.
XX
SO
    Sequence 7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other;
 Query Match
                     63.9%; Score 334.4; DB 24; Length 7260;
 Best Local Similarity 84.6%; Pred. No. 5.7e-88;
 Matches 445; Conservative 0; Mismatches 26; Indels
                                                    55; Gaps
                                                               4;
Qу
         1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGGAGAC 60
           Db
        311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370
Qу
         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCCACCTCAG 120
           Db
        371 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430
        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
Qу
           431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490
Db
        Qу
           491 TGCGCACCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 550
Db
        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
Qу
           551 ATGCCCAAGACCCAG----- 565
Db
        301 AGAAGGAAAGGAAGTACATTTGAAGAACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
Qу
                 566 -----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 618
Db
        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
Qу
           619 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 678
Db
        421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
Qy
           Db
        679 CTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 738
        479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
Qу
```

739 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTC 784

RESULT 14 ABN97244 ID ABN97244 standard; DNA; 7260 BP. XX AC ABN97244; XX 13-AUG-2002 (first entry) DTXX DE Gene #3742 used to diagnose liver cancer. XX ΚŴ Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic; KW metastatic liver tumour; cytostatic; expression profile; disease state; KW disease progression; drug toxicity; drug efficacy; drug metabolism. XX OS Homo sapiens. XX WO200229103-A2. PN XX PD11-APR-2002. XX PF 02-OCT-2001; 2001WO-US30589. XX PR 02-OCT-2000; 2000US-237054P. XX PA (GENE-) GENE LOGIC INC. XX PΙ Horne D, Alvares C, Peres-Da-Silva S, Vockley JG; XX DR WPI; 2002-426119/45. XX PTDiagnosing and detecting the progression of liver cancer, PThepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes in a PТ liver tissue sample XX PS Claim 1; SEQ ID NO 3742; 298pp; English. XX CC The invention relates to a novel method for diagnosing and detecting the CC progression of liver cancer, hepatocellular carcinoma or metastatic liver CC tumour in a patient, and differentiating metastatic liver cancer from CC hepatocellular carcinoma in a patient, involving detecting the level of CC expression of two or more genes represented in ABN93503-ABN97455 in a CC tissue sample. The method of the invention has hepatotropic, and CC cytostatic activity. The method is useful for diagnosing and detecting CC the progression of liver cancer, hepatocellular carcinoma and metastatic CC liver carcinoma in a patient. The method is useful for identifying CC expression profiles which serve as useful diagnostic markers as well as CC markers that can be used to monitor disease states, disease progression, CC drug toxicity, drug efficacy and drug metabolism. CC Note: The sequence data for this patent did not form part of the printed CC specification, but was obtained in electronic format directly from WIPO CC at ftp.wipo.int/pub/published pct sequences. XX

```
Query Match
                    63.9%; Score 334.4; DB 24; Length 7260;
  Best Local Similarity
                    84.6%; Pred. No. 5.7e-88;
 Matches 445; Conservative
                         0; Mismatches
                                      26; Indels
                                                 55; Gaps
                                                           4;
Qy
         1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGGAGAC 60
           Db
        311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370
Qy
        61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
           Db
        371 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430
Qу
        121 ACAGGCATCGTGGATGATGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
           431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490
Db
Ov
        181 TGTGCACCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCCAGCGCCACACCGAC 240
           491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCCACACCGAC 550
Db
Qy
        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
           551 ATGCCCAAGACCCAG----- 565
Db
Qy
        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
                Db
        566 -----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 618
        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
Qy
           619 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 678
Db
        421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
Qy
           679 CTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 738
Db
        479 TTCAAAGAT-GGCATTTCCCCCCAATGAAATACACAAGTAAACATTC 523
Qy
           739 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTC 784
Db
RESULT 15
ABK64812
ID
   ABK64812 standard; DNA; 7260 BP.
XX
AC
   ABK64812;
XX
DT
    18-JUN-2002 (first entry)
XX
DE
   Human benign prostatic hyperplasia gene #707.
XX
KW
    Human; benign prostatic hyperplasia; BPH; prostate cancer; gene; ds.
XX
OS
   Homo sapiens.
XX
```

```
PN
    WO200212440-A2.
XX
PD
     14-FEB-2002.
XX
PF
     07-AUG-2001; 2001WO-US24708.
XX
PR
     07-AUG-2000; 2000US-223323P.
PR
     05-JUN-2001; 2001US-0873319.
XX
     (GENE-) GENE LOGIC INC.
PA
     (NISB ) JAPAN TOBACCO INC.
PA
XX
PΙ
    Munger WE, Kulkarni P, Getzenberg RH, Waga I, Yamamoto J;
XX
    WPI; 2002-257476/30.
DR
XX
PΤ
     Identifying drugs for and diagnosing benign prostatic hyperplasia, by
PT
     detecting expression levels of one or more genes in prostate cells from
PТ
     patient that are differentially regulated compared to normal prostate
PT
     cells -
XX
PS
    Disclosure; Page 391-393; 444pp; English.
XX
CC
    The invention relates to a method of diagnosing (I) the onset or
CC
    progression of benign prostatic hyperplasia (BPH), or screening (II) for
CC
    or identifying an agent that modulates the onset or progression of BPH.
CC
    The method is based on changes in gene expression in BPH tissue isolated
CC
     from patients exhibiting different clinical states of prostate
CC
    hyperplasia as compared to normal prostate tissue. (I) comprises
CC
     detecting the expression levels of one or more genes in prostate cells
CC
     from the subject that are differentially regulated compared to normal
CC
    prostate cells. (II) comprises preparing a first gene expression profile
CC
     of BPH cells or BPH-like cell population, exposing the cells to the
CC
     agent, preparing a second gene expression profile of the agent exposed
CC
     cells, and comparing the first and second gene expression profiles.
CC
     (I) is useful for diagnosing the onset or progression of BPH. (II) is
CC
    useful for identifying an agent that modulates the onset or progression
CC
    of BPH. The methods are useful to present information identifying
CC
    the expression level in a tissue or cells, by comparing the expression
CC
     level of genes given in the specification in the tissue or cells to the
CC
    level of expression of gene in the database, and displaying the
CC
    expression levels of at least one gene in the tissue or cell sample
CC
     compared to the expression level in BPH. Agents using (II) are useful for
CC
     treating BPH or prostate cancer. ABK64106-ABK64860 represent human
CC
    benign prostatic hyperplasia gene sequences of the invention.
XX
SQ
     Sequence 7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other;
  Query Match
                         63.9%; Score 334.4; DB 24;
                                                       Length 7260;
  Best Local Similarity
                         84.6%; Pred. No. 5.7e-88;
 Matches 445; Conservative
                                0; Mismatches
                                                 26; Indels
                                                                            4;
Qy
            1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGGAGAC 60
              Db
         311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370
          61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
Qу
```

Db	371	AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG	430
Qу	121	ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC	180
Db	431	ACAGGCATCGTGGATGAGTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT	490
Qу	181	TGTGCACCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCG	240
Db	491	TGCGCACCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC	550
Qу	241	ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG	300
Db .	551	ATGCCCAAGACCCAG	565
QУ	301	AGAAGGAAAGGAACTTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA	360
Db	566	AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA	618
Qγ	361	CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG	420
Db	619	CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG	678
Qу	421	CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT	478
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Search completed: December 13, 2003, 06:03:51 Job time : 211.995 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 06:03:55; Search time 48.3585 Seconds

(without alignments)

4773.589 Million cell updates/sec

Title:

US-09-852-261-5

Perfect score: 523

Sequence: 1 ggaccggagacgctctgcgg.....aaatacacaagtaaacattc 523

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched:

569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

Database : Issued Patents NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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332.8	63.6	777	3	US-09-142-583A-10	Sequence 10, Appl
331.2	63.3	622	6	5405942-2	Patent No. 5405942
274.6	52.5	5707	2	US-08-472-809B-8	Sequence 8, Appli
274.6	52.5	6345	2	US-08-472-809B-7	Sequence 7, Appli
234.4	44.8	357	6	5405942-13	Patent No. 5405942
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ALIGNMENTS

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; Sequence 3, Application US/09142583A
 Patent No. 6221842
    GENERAL INFORMATION:
         APPLICANT: GOLDSPINK, GEOFFREY
         TITLE OF INVENTION: METHOD OF TREATING MUSCULAR DISORDERS
;
         NUMBER OF SEQUENCES: 11
;
         CORRESPONDENCE ADDRESS:
              ADDRESSEE: NIXON & VANDERHYE P.C.
              STREET: 1100 NORTH GLEBE ROAD
              CITY: ARLINGTON
              STATE: VA
              COUNTRY: USA
              ZIP: 22201
         COMPUTER READABLE FORM:
              MEDIUM TYPE: Floppy disk
              COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS
           SOFTWARE: PatentIn Release #1.0, Version #1.25
       CURRENT APPLICATION DATA:
           APPLICATION NUMBER: US/09/142,583A
           FILING DATE: 29-Oct-1998
           CLASSIFICATION: <Unknown>
       PRIOR APPLICATION DATA:
           APPLICATION NUMBER: WO PCT/GB97/00658
           FILING DATE: 11-MAR-1997
           APPLICATION NUMBER: GB 9605124.8
           FILING DATE: 11-MAR-1996
       ATTORNEY/AGENT INFORMATION:
           NAME: SADOFF, B. J.
           REGISTRATION NUMBER: 36663
           REFERENCE/DOCKET NUMBER: 117-263
       TELECOMMUNICATION INFORMATION:
           TELEPHONE: 7038164000
           TELEFAX: 7038164100
   INFORMATION FOR SEQ ID NO: 3:
       SEQUENCE CHARACTERISTICS:
           LENGTH: 553 base pairs
           TYPE: nucleic acid
           STRANDEDNESS: both
           TOPOLOGY: linear
       MOLECULE TYPE: cDNA
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           NAME/KEY: CDS
           LOCATION: 1..363
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 Best Local Similarity
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 Matches 523; Conservative
                          0; Mismatches
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; Sequence 5, Application US/09142583A
; Patent No. 6221842
   GENERAL INFORMATION:
        APPLICANT: GOLDSPINK, GEOFFREY
        TITLE OF INVENTION: METHOD OF TREATING MUSCULAR DISORDERS
        NUMBER OF SEQUENCES: 11
        CORRESPONDENCE ADDRESS:
            ADDRESSEE: NIXON & VANDERHYE P.C.
            STREET: 1100 NORTH GLEBE ROAD
            CITY: ARLINGTON
            STATE: VA
            COUNTRY: USA
            ZIP: 22201
        COMPUTER READABLE FORM:
            MEDIUM TYPE: Floppy disk
            COMPUTER: IBM PC compatible
            OPERATING SYSTEM: PC-DOS/MS-DOS
            SOFTWARE: PatentIn Release #1.0, Version #1.25
        CURRENT APPLICATION DATA:
            APPLICATION NUMBER: US/09/142,583A
            FILING DATE: 29-Oct-1998
            CLASSIFICATION: <Unknown>
        PRIOR APPLICATION DATA:
            APPLICATION NUMBER: WO PCT/GB97/00658
            FILING DATE: 11-MAR-1997
            APPLICATION NUMBER: GB 9605124.8
            FILING DATE: 11-MAR-1996
        ATTORNEY/AGENT INFORMATION:
            NAME: SADOFF, B. J.
            REGISTRATION NUMBER: 36663
            REFERENCE/DOCKET NUMBER: 117-263
        TELECOMMUNICATION INFORMATION:
            TELEPHONE: 7038164000
            TELEFAX: 7038164100
   INFORMATION FOR SEQ ID NO: 5:
        SEQUENCE CHARACTERISTICS:
            LENGTH: 553 base pairs
            TYPE: nucleic acid
            STRANDEDNESS: both
            TOPOLOGY: linear
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MOLECULE TYPE: cDNA
      FEATURE:
          NAME/KEY: CDS
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                        Score 523; DB 3; Length 553;
 Best Local Similarity
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; Sequence 10, Application US/09142583A
 Patent No. 6221842
  GENERAL INFORMATION:
      APPLICANT: GOLDSPINK, GEOFFREY
      TITLE OF INVENTION: METHOD OF TREATING MUSCULAR DISORDERS
      NUMBER OF SEQUENCES: 11
      CORRESPONDENCE ADDRESS:
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ADDRESSEE: NIXON & VANDERHYE P.C.
            STREET: 1100 NORTH GLEBE ROAD
            CITY: ARLINGTON
            STATE: VA
            COUNTRY: USA
            ZIP: 22201
       COMPUTER READABLE FORM:
            MEDIUM TYPE: Floppy disk
            COMPUTER: IBM PC compatible
            OPERATING SYSTEM: PC-DOS/MS-DOS
            SOFTWARE: PatentIn Release #1.0, Version #1.25
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            FILING DATE: 29-Oct-1998
            CLASSIFICATION: <Unknown>
       PRIOR APPLICATION DATA:
            APPLICATION NUMBER: WO PCT/GB97/00658
            FILING DATE: 11-MAR-1997
            APPLICATION NUMBER: GB 9605124.8
            FILING DATE: 11-MAR-1996
       ATTORNEY/AGENT INFORMATION:
            NAME: SADOFF, B. J.
            REGISTRATION NUMBER: 36663
            REFERENCE/DOCKET NUMBER: 117-263
       TELECOMMUNICATION INFORMATION:
            TELEPHONE: 7038164000
            TELEFAX: 7038164100
   INFORMATION FOR SEQ ID NO: 10:
       SEQUENCE CHARACTERISTICS:
            LENGTH: 777 base pairs
            TYPE: nucleic acid
            STRANDEDNESS: both
            TOPOLOGY: linear
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            NAME/KEY: CDS
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    APPLICANT: BELL, GRAEME I.; RALL, LESLIE B.; MERRYWEATHER,
; JAMES P.
   TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS
; I AND II
   NUMBER OF SEQUENCES: 16
    CURRENT APPLICATION DATA:
     APPLICATION NUMBER: US/07/65,673
     FILING DATE: 16-JUN-1987
    PRIOR APPLICATION DATA:
     APPLICATION NUMBER: 630,557
     FILING DATE: 19-JUL-1984
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 Best Local Similarity 68.3%; Pred. No. 2.8e-94;
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; Sequence 8, Application US/08472809B
 Patent No. 5925564
  GENERAL INFORMATION:
   APPLICANT: Schwartz, Robert J.
   APPLICANT: DeMayo, Franco J.
   APPLICANT: O'Malley, Bert W.
   TITLE OF INVENTION: Expression Vector Systems and
   TITLE OF INVENTION: Method of Use
   NUMBER OF SEQUENCES: 8
   CORRESPONDENCE ADDRESS:
   ADDRESSEE: Lyon & Lyon
     STREET: 633 West Fifth Street STREET: Suite 4700
     CITY: Los Angeles
     STATE: California
     COUNTRY: U.S.A.
     ZIP: 90071-2066
   COMPUTER READABLE FORM:
     MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
     MEDIUM TYPE: storage
     COMPUTER: IBM Compatible
     OPERATING SYSTEM: IBM P.C. DOS 5.0
     SOFTWARE: Word Perfect 5.1
   CURRENT APPLICATION DATA:
     APPLICATION NUMBER: US/08/472,809B
     FILING DATE: June 7, 1995
     CLASSIFICATION: 435
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/209,846

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FILING DATE: March 9, 1994
     APPLICATION NUMBER: 07/789,919
     FILING DATE: No. 5925564ember 6, 1991
    ATTORNEY/AGENT INFORMATION:
     NAME: Warburg, Richard J.
     REGISTRATION NUMBER: 32,327
     REFERENCE/DOCKET NUMBER: 214/212
    TELECOMMUNICATION INFORMATION:
     TELEPHONE: (213) 489-1600
     TELEFAX: (213) 955-0440
     TELEX: 67-3510
  INFORMATION FOR SEQ ID NO: 8:
    SEQUENCE CHARACTERISTICS:
     LENGTH: 5707 bases
     TYPE: nucleic acid
     STRANDEDNESS: double
     TOPOLOGY: linear
   MOLECULE TYPE: cDNA
US-08-472-809B-8
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                    52.5%; Score 274.6; DB 2; Length 5707;
 Best Local Similarity 82.2%; Pred. No. 5.3e-76;
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        61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
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          Db
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          973 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 1032
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       241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
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RESULT 6
US-08-472-809B-7
; Sequence 7, Application US/08472809B
; Patent No. 5925564
  GENERAL INFORMATION:
    APPLICANT: Schwartz, Robert J.
    APPLICANT: DeMayo, Franco J.
    APPLICANT: O'Malley, Bert W.
    TITLE OF INVENTION: Expression Vector Systems and
    TITLE OF INVENTION: Method of Use
    NUMBER OF SEQUENCES: 8
    CORRESPONDENCE ADDRESS:
      ADDRESSEE: Lyon & Lyon
      STREET: 633 West Fifth Street
      STREET: Suite 4700
      CITY: Los Angeles
      STATE: California
      COUNTRY: U.S.A.
      ZIP: 90071-2066
    COMPUTER READABLE FORM:
      MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
      MEDIUM TYPE: storage
      COMPUTER: IBM Compatible
      OPERATING SYSTEM: IBM P.C. DOS 5.0
      SOFTWARE: Word Perfect 5.1
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/08/472,809B
      FILING DATE: June 7, 1995
      CLASSIFICATION: 435
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER: 08/209,846
      FILING DATE: March 9, 1994
      APPLICATION NUMBER: 07/789,919
      FILING DATE: No. 5925564ember 6, 1991
    ATTORNEY/AGENT INFORMATION:
      NAME: Warburg, Richard J.
      REGISTRATION NUMBER: 32,327
      REFERENCE/DOCKET NUMBER:
                             214/212
    TELECOMMUNICATION INFORMATION:
      TELEPHONE: (213) 489-1600
      TELEFAX: (213) 955-0440
;
      TELEX: 67-3510
  INFORMATION FOR SEQ ID NO: 7:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 6345 bases
      TYPE: nucleic acid
      STRANDEDNESS: double
      TOPOLOGY: linear
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US-08-472-809B-7
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 Best Local Similarity 82.2%; Pred. No. 5.6e-76;
 Matches 351; Conservative
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       241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
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       3942 ATGCCCAAGACCCAG----- 3956
Db
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       301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
                Db
       3957 -----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 4009
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Qy
           Db
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Qy
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       4070 GGCTGCA 4076
RESULT 7
5405942-13
; Patent No. 5405942
   APPLICANT: BELL, GRAEME I.; RALL, LESLIE B.; MERRYWEATHER,
   TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS
; I AND II
   NUMBER OF SEQUENCES: 16
   CURRENT APPLICATION DATA:
     APPLICATION NUMBER: US/07/65,673
     FILING DATE: 16-JUN-1987
   PRIOR APPLICATION DATA:
     APPLICATION NUMBER: 630,557
     FILING DATE: 19-JUL-1984
;SEQ ID NO:13:
     LENGTH: 357
5405942-13
                    44.8%; Score 234.4; DB 6;
 Query Match
                                          Length 357;
 Best Local Similarity
                    93.8%; Pred. No. 5.1e-64;
 Matches 244; Conservative
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                                          Indels
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         1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
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          Db
       103 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 162
       121 ACAGGCATCGTGGATGATGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
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          Db
       163 ACAGGTATCGTGGATGATGTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 222
       Qу
          Db
       223 TGCGCACCCTCAGGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 282
       241 ATGCCCAAGACTCAGAAGTA 260
Qy
          283 ATGCCCAAGACCCAGAAGGA 302
Db
RESULT 8
5405942-9
; Patent No. 5405942
   APPLICANT: BELL, GRAEME I.; RALL, LESLIE B.; MERRYWEATHER.
   TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS
;I AND II
   NUMBER OF SEQUENCES: 16
   CURRENT APPLICATION DATA:
     APPLICATION NUMBER: US/07/65,673
     FILING DATE: 16-JUN-1987
   PRIOR APPLICATION DATA:
     APPLICATION NUMBER: 630,557
     FILING DATE: 19-JUL-1984
;SEQ ID NO:9:
     LENGTH: 357
5405942-9
                   44.5%; Score 232.8; DB 6; Length 357;
 Query Match
                  76.5%; Pred. No. 1.6e-63;
 Best Local Similarity
 Matches 199; Conservative 44; Mismatches 17;
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       121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
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          163 ACAGGUAUCGUGGAUGAUGUGUUUCCGGAGCUGUGAUCUAAGGAGGCUGGAGAUGUAU 222
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Qy
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RESULT 9
5405942-7
; Patent No. 5405942
    APPLICANT: BELL, GRAEME I.; RALL, LESLIE B.; MERRYWEATHER,
; JAMES P.
    TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS
; I AND II
    NUMBER OF SEQUENCES: 16
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/07/65,673
      FILING DATE: 16-JUN-1987
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER: 630,557
      FILING DATE: 19-JUL-1984
;SEO ID NO:7:
      LENGTH: 210
5405942-7
 Query Match
                       36.6%; Score 191.4; DB 6; Length 210;
 Best Local Similarity 75.1%; Pred. No. 1.2e-50;
 Matches 157; Conservative 41; Mismatches 11; Indels
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Qy
        121 ACAGGCATCGTGGATGATGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
            Db
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        181 UGCGCACCCCUCAAGCCUGCCAAGUCAGC 209
RESULT 10
5405942-11
; Patent No. 5405942
    APPLICANT: BELL, GRAEME I.; RALL, LESLIE B.; MERRYWEATHER,
; JAMES P.
    TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS
;I AND II
    NUMBER OF SEQUENCES: 16
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/07/65,673
      FILING DATE: 16-JUN-1987
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER: 630,557
      FILING DATE: 19-JUL-1984
;SEQ ID NO:11:
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LENGTH: 210
5405942-11
 Query Match
                       36.6%; Score 191.4; DB 6; Length 210;
 Best Local Similarity 94.7%; Pred. No. 1.2e-50;
 Matches 198; Conservative
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RESULT 11
US-09-255-829-13
; Sequence 13, Application US/09255829
; Patent No. 6461617
  GENERAL INFORMATION:
    APPLICANT: Shone, Clifford Charles
    APPLICANT: Quinn, Conrad Padraig
APPLICANT: Foster, Keith Alan
    TITLE OF INVENTION: Recombinant Toxin Fragments
    NUMBER OF SEQUENCES: 29
    CORRESPONDENCE ADDRESS:
      ADDRESSEE: STERNE, KESSLER, GOLDSTEIN, & FOX P.L.L.C.
      STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
      CITY: WASHINGTON
      STATE: DC
      COUNTRY: USA
      ZIP: 20005-3934
    COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/09/255,829
      FILING DATE: 23-FEB-1999
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER: PCT/GB97/02273
      FILING DATE: 22-AUG-1997
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 08/782,893
      FILING DATE: 27-DEC-1996
    ATTORNEY/AGENT INFORMATION:
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NAME: ESMOND, ROBERT W.

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REGISTRATION NUMBER: 32,893
      REFERENCE/DOCKET NUMBER: 1581.0130002
    TELECOMMUNICATION INFORMATION:
      TELEPHONE: 202-371-2600
      TELEFAX: 202-371-2540
  INFORMATION FOR SEQ ID NO: 13:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 2862 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: double
      TOPOLOGY: linear
    MOLECULE TYPE: DNA (genomic)
    FEATURE:
      NAME/KEY: CDS
      LOCATION: 1..2862
US-09-255-829-13
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RESULT 12
5405942-15
;Patent No. 5405942
    APPLICANT: BELL, GRAEME I.; RALL, LESLIE B.; MERRYWEATHER,
; JAMES P.
    TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS
; I AND II
    NUMBER OF SEQUENCES: 16
    CURRENT APPLICATION DATA:
     APPLICATION NUMBER: US/07/65,673
     FILING DATE: 16-JUN-1987
    PRIOR APPLICATION DATA:
     APPLICATION NUMBER: 630,557
     FILING DATE: 19-JUL-1984
;SEQ ID NO:15:
      LENGTH: 210
5405942-15
                   36.3%; Score 189.8; DB 6; Length 210;
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         181 UGCGCACCCCUCAGGCCUGCCAAGUCAGC 209
RESULT 13
US-08-308-196A-1
; Sequence 1, Application US/08308196A
; Patent No. 5612198
  GENERAL INFORMATION:
    APPLICANT: Brierley, Russell A.
    APPLICANT: Davis, Geneva R.
    APPLICANT: Holtz, Gregory C.
    APPLICANT: Gleeson, Martin A.
    APPLICANT: Howard, Bradley D.
    TITLE OF INVENTION: Production of Insulin-Like Growth
TITLE OF INVENTION: Factor-1 in Methylotrophic Yeast Cells
    NUMBER OF SEQUENCES: 17
    CORRESPONDENCE ADDRESS:
     ADDRESSEE: Brown, Martin, Haller & McClain
      STREET: 1660 Union Street
      CITY: San Diego
      STATE: California
      COUNTRY: USA
      ZIP: 92101-2926
    COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: PatentIn Release #1.0, Version #1.25
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/08/308,196A
      FILING DATE: 09-SEPT-1994
    PRIOR APPLICATION DATA:
     APPLICATION NUMBER: US 07/983,523
      FILING DATE: 03-MAR-1993
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 07/578,728
     FILING DATE: 04-SEP-1990
    ATTORNEY/AGENT INFORMATION:
     NAME: Seidman, Stephanie L.
      REGISTRATION NUMBER: 33,779
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REFERENCE/DOCKET NUMBER:
                             51875
    TELECOMMUNICATION INFORMATION:
      TELEPHONE: (619)238-0999
      TELEFAX: (619)238-0062
  INFORMATION FOR SEQ ID NO: 1:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 240 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: double
      TOPOLOGY: unknown
    MOLECULE TYPE: cDNA
    FEATURE:
      NAME/KEY: CDS
      LOCATION: 14..232
US-08-308-196A-1
 Query Match
                      35.4%; Score 185.2; DB 1; Length 240;
 Best Local Similarity
                      91.6%; Pred. No. 1.1e-48;
 Matches 196; Conservative
                            0; Mismatches 18; Indels
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Db
RESULT 14
PCT-US91-06452-1
; Sequence 1, Application PC/TUS9106452
  GENERAL INFORMATION:
    APPLICANT: Brierley, Russell A.
    APPLICANT: Davis, Geneva R.
    APPLICANT: Holtz, Gregory C.
    APPLICANT: Gleeson, Martin A.
    APPLICANT: Bradley, D. H.
    TITLE OF INVENTION: Production of Insulin-Like Growth
    TITLE OF INVENTION: Factor-1 in Methylotrophic Yeast Cells
    NUMBER OF SEQUENCES: 12
    CORRESPONDENCE ADDRESS:
      ADDRESSEE: Fitch, Even, Tabin & Flannery
      STREET: 135 South LaSalle Street, Suite 900
     CITY: Chicago
      STATE: Illinois
     COUNTRY: USA
      ZIP: 60603
    COMPUTER READABLE FORM:
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MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: PatentIn Release #1.0, Version #1.25
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER: PCT/US91/06452
      FILING DATE: 19910409
      CLASSIFICATION: 435
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 07/578,728
      FILING DATE: 04-SEP-1990
    ATTORNEY/AGENT INFORMATION:
      NAME: Seidman, Stephanie L.
      REGISTRATION NUMBER: 33,779
      REFERENCE/DOCKET NUMBER:
    TELECOMMUNICATION INFORMATION:
      TELEPHONE: (619)552-1311
      TELEFAX: (619)552-0095
  INFORMATION FOR SEQ ID NO: 1:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 240 base pairs
      TYPE: NUCLEIC ACID
      STRANDEDNESS: double
      TOPOLOGY: unknown
    MOLECULE TYPE: cDNA
    FEATURE:
      NAME/KEY: CDS
      LOCATION: 14..232
PCT-US91-06452-1
 Query Match
                       35.4%; Score 185.2; DB 5; Length 240;
 Best Local Similarity
                      91.6%; Pred. No. 1.1e-48;
 Matches 196; Conservative
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          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
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Db
        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
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Qy
            Db
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RESULT 15
US-09-029-267-13
; Sequence 13, Application US/09029267
; Patent No. 6107057
  GENERAL INFORMATION:
    APPLICANT: Crawford, Kenneth
    APPLICANT: Zaror, Isabel
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APPLICANT: Innis, Michael
    TITLE OF INVENTION: Pichia Secretory Leader for Protein
    TITLE OF INVENTION: Expression
    NUMBER OF SEQUENCES: 40
    CORRESPONDENCE ADDRESS:
      ADDRESSEE: Chiron Corporation
      STREET: 4560 Horton Street
      CITY: Emeryville
      STATE: California
      COUNTRY: United States
      ZIP: 94608
    COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: PatentIn Release #1.0, Version #1.30
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/09/029,267
      FILING DATE:
      CLASSIFICATION:
    ATTORNEY/AGENT INFORMATION:
      NAME: Chung, Ling-Fong
      REGISTRATION NUMBER: 36,482
      REFERENCE/DOCKET NUMBER: 1165.100
    TELECOMMUNICATION INFORMATION:
      TELEPHONE: (510) 601-2704
      TELEFAX: (510) 655-3542
  INFORMATION FOR SEQ ID NO: 13:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 390 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear
    MOLECULE TYPE: other nucleic acid
      DESCRIPTION: /desc = "Synthetic"
US-09-029-267-13
 Query Match
                      35.4%; Score 185.2; DB 3; Length 390;
 Best Local Similarity 91.6%; Pred. No. 1.5e-48;
 Matches 196; Conservative
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Qу
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Title:

US-09-852-261-5

Perfect score: 523

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched:

2201672 seqs, 1661799599 residues

Total number of hits satisfying chosen parameters:

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result Query

> No. Score Match Length DB ID

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	4	356.8	68.2	539	9	US-09-852-261-3	Sequence 3, Appli
	5	349.4	66.8	651	15	US-10-161-088-1	Sequence 1, Appli
	6	334.4	63.9	7260	10	US-09-919-497-24	Sequence 24, Appl
	7	334.4	63.9	7260	10	US-09-880-107-3739	Sequence 3739, Ap
	8	334.4	63.9	7260	13	US-09-873-319-707	Sequence 707, App
	9	334.4	63.9	7260	13	US-09-960-706-1066	Sequence 1066, Ap
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С	34	75.4	14.4	447	14	US-10-025-380-917	Sequence 917, App
С	35	75.2	14.4	437	15	US-10-066-543-663	Sequence 663, App
С	36	75.2	14.4	493	15	US-10-066-543-997	Sequence 997, App
С	37	75.2	14.4	518	15	US-10-066-543-1040	Sequence 1040, Ap
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С	40	75.2	14.4	549	15	US-10-066-543-478	Sequence 478, App
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С	45	75.2	14.4	579	15	US-10-066-543-1094	Sequence 1094, Ap

ALIGNMENTS

RESULT 1

US-09-852-261-5

- ; Sequence 5, Application US/09852261 ; Patent No. US20020083477A1
- ; GENERAL INFORMATION:
- ; APPLICANT: GOLDSPINK, GEOFFREY

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APPLICANT: TERENGHI, GIORGIO
  TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
  FILE REFERENCE: 117-351
  CURRENT APPLICATION NUMBER: US/09/852,261
  CURRENT FILING DATE: 2001-05-10
  PRIOR APPLICATION NUMBER: GB 0011278.9
  PRIOR FILING DATE: 2000-05-10
  NUMBER OF SEQ ID NOS: 14
  SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 5
  LENGTH: 523
  TYPE: DNA
  ORGANISM: Oryctolagus cuniculus
US-09-852-261-5
 Query Match
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 Best Local Similarity
                  100.0%; Pred. No. 1.9e-161;
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US-09-852-261-1
; Sequence 1, Application US/09852261
; Patent No. US20020083477A1
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  APPLICANT: GOLDSPINK, GEOFFREY
  APPLICANT: TERENGHI, GIORGIO
  TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
  FILE REFERENCE: 117-351
  CURRENT APPLICATION NUMBER: US/09/852,261
  CURRENT FILING DATE: 2001-05-10
  PRIOR APPLICATION NUMBER: GB 0011278.9
  PRIOR FILING DATE: 2000-05-10
  NUMBER OF SEQ ID NOS: 14
  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
   LENGTH: 517
   TYPE: DNA
   ORGANISM: Homo sapiens
US-09-852-261-1
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 Best Local Similarity 96.2%; Pred. No. 3.8e-143;
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RESULT 3
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  APPLICANT: TERENGHI, GIORGIO
  TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
  FILE REFERENCE: 117-351
  CURRENT APPLICATION NUMBER: US/09/852,261
  CURRENT FILING DATE: 2001-05-10
  PRIOR APPLICATION NUMBER: GB 0011278.9
  PRIOR FILING DATE: 2000-05-10
  NUMBER OF SEQ ID NOS: 14
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; Patent No. US20020083477A1
; GENERAL INFORMATION:
  APPLICANT: GOLDSPINK, GEOFFREY
  APPLICANT: TERENGHI, GIORGIO
  TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
  FILE REFERENCE: 117-351
  CURRENT APPLICATION NUMBER: US/09/852,261
  CURRENT FILING DATE: 2001-05-10
  PRIOR APPLICATION NUMBER: GB 0011278.9
  PRIOR FILING DATE: 2000-05-10
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; Publication No. US20030077761A1
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  APPLICANT: Parrow, Vendela
  APPLICANT: Rosengren, Linda
  TITLE OF INVENTION: NEW METHODS
  FILE REFERENCE: 13425-111001
  CURRENT APPLICATION NUMBER: US/10/161,088
  CURRENT FILING DATE: 2002-05-31
  PRIOR APPLICATION NUMBER: SE 0101934-8
  PRIOR FILING DATE: 2001-06-01
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; Sequence 24, Application US/09919497
; Patent No. US20020106662A1
: GENERAL INFORMATION:
  APPLICANT: Mutter, George L.
  TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
  FILE REFERENCE: B0801/7225
  CURRENT APPLICATION NUMBER: US/09/919,497
  CURRENT FILING DATE: 2001-07-31
  PRIOR APPLICATION NUMBER: US 60/221,735
  PRIOR FILING DATE: 2000-07-31
  NUMBER OF SEQ ID NOS: 100
  SOFTWARE: PatentIn version 3.0
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   TYPE: DNA
   ORGANISM: Homo sapiens
US-09-919-497-24
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 Best Local Similarity
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; Sequence 3739, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
  APPLICANT: Horne, Darci T.
  APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
  APPLICANT: Gene Logic, Inc.
  TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
  FILE REFERENCE: 44921-5028-WO
  CURRENT APPLICATION NUMBER: US/09/880,107
  CURRENT FILING DATE: 2001-06-14
  PRIOR APPLICATION NUMBER: US 60/211,379
  PRIOR FILING DATE: 2000-06-14
  PRIOR APPLICATION NUMBER: US 60/237,054
  PRIOR FILING DATE: 2000-10-02
  NUMBER OF SEQ ID NOS: 3950
  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3739
  LENGTH: 7260
   TYPE: DNA
   ORGANISM: Homo sapiens
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Qу	61	AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG	120
Db	371	AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG	430
Qу	121	ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC	180
Db	431	ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT	490
Qу	181	TGTGCACCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCG	240
Db		TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC	
Qу	241	ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG	
Db		ATGCCCAAGACCCAG	565
Qy		AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA	
Db		AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA	
QУ		CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG	
Db		CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG	
Qу		CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT	
Db		CICIGCACGAGITACCIGITAAACITTOOMAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	738
Qу		TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523	
Db	739	TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTC 784	

RESULT 8

US-09-873-319-707

- ; Sequence 707, Application US/09873319A
- ; Publication No. US20030134324A1
- ; GENERAL INFORMATION:
- ; APPLICANT: Munger, William E.
- ; APPLICANT: Kulkarni, Prakash
- ; APPLICANT: Getzenberg, Robert H.
- ; APPLICANT: Waga, Iwao
- ; APPLICANT: Yamamoto, Jun
- ; TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic
- ; TITLE OF INVENTION: Hyperplasia Using Gene Expression Profiles
- ; FILE REFERENCE: 44921-5029-US
- ; CURRENT APPLICATION NUMBER: US/09/873,319A
- ; CURRENT FILING DATE: 2001-06-05
- ; EARLIER APPLICATION NUMBER: US 60/223,323
- ; EARLIER FILING DATE: 2000-08-07
- ; NUMBER OF SEQ ID NOS: 755
- ; SOFTWARE: PatentIn Ver. 2.1
- ; SEQ ID NO 707

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LENGTH: 7260
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   TYPE: DNA
   ORGANISM: Homo sapiens
   FEATURE:
   OTHER INFORMATION: Genbank Accession No. US20030134324A1 X57025
US-09-873-319-707
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                   84.6%; Pred. No. 9e-99;
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 Matches 445; Conservative
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          311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370
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          431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490
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          619 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 678
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          679 CTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 738
Db
       479 TTCAAAGAT-GGCATTTCCCCCCAATGAAATACACAAGTAAACATTC 523
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RESULT 9
US-09-960-706-1066
; Sequence 1066, Application US/09960706
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- ; Publication No. US20030134280A1
- ; GENERAL INFORMATION:
- APPLICANT: Munger, William E.
- TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplasia Using
- ; TITLE OF INVENTION: Gene Expression Profiles

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FILE REFERENCE: 44921-5029-01US
  CURRENT APPLICATION NUMBER: US/09/960,706
  CURRENT FILING DATE: 2001-09-24
  PRIOR APPLICATION NUMBER: 60/223,323
  PRIOR FILING DATE: 2000-08-07
  PRIOR APPLICATION NUMBER: 09/873,319
  PRIOR FILING DATE: 2001-06-05
  NUMBER OF SEQ ID NOS: 1124
  SOFTWARE: PatentIn Ver. 2.1
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  LENGTH: 7260
   TYPE: DNA
   ORGANISM: Homo sapiens
   FEATURE:
   OTHER INFORMATION: Genbank Accession No. US20030134280A1 X57025
US-09-960-706-1066
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 Best Local Similarity 84.6%; Pred. No. 9e-99;
 Matches 445: Conservative
                         0; Mismatches
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                                         Indels
                                                    Gaps
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          311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370
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Qу
           679 CTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 738
Db
       479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
Qу
           739 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTC 784
Db
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RESULT 10
US-10-136-639-4
; Sequence 4, Application US/10136639
; Publication No. US20030072761A1
; GENERAL INFORMATION:
  APPLICANT: LeBowitz, Jonathan
  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TARGETING PROTEINS ACROSS
THE BLOOD BRAIN
  TITLE OF INVENTION: BARRIER
  FILE REFERENCE: SYM-008
  CURRENT APPLICATION NUMBER: US/10/136,639
  CURRENT FILING DATE: 2002-09-06
  PRIOR APPLICATION NUMBER: US 60/329,650
  PRIOR FILING DATE: 2001-10-16
  NUMBER OF SEQ ID NOS: 4
  SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
   LENGTH: 7260
   TYPE: DNA
   ORGANISM: Homo sapiens
US-10-136-639-4
                   63.9%; Score 334.4; DB 15; Length 7260;
 Query Match
 Best Local Similarity 84.6%; Pred. No. 9e-99;
 Matches 445; Conservative
                         0; Mismatches
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Qу
          311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGGAGAC 370
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        61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
Qу
          371 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430
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       121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
Qу
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               566 -----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 618
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       361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
Qу
           619 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 678
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       421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
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679 CTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 738
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Qу
           739 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTC 784
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RESULT 11
US-10-207-655-54
; Sequence 54, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
  APPLICANT: Ledbetter, Jeffrey A.
  APPLICANT: Hayden-Ledbetter, Martha S.
  TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
  FILE REFERENCE: 390069.401C1
  CURRENT APPLICATION NUMBER: US/10/207,655
  CURRENT FILING DATE: 2002-07-25
  NUMBER OF SEO ID NOS: 426
  SOFTWARE: PatentIn version 3.0
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   LENGTH: 725
   TYPE: DNA
   ORGANISM: Homo sapiens
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                    63.6%; Score 332.8; DB 15; Length 725;
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 Best Local Similarity 84.4%; Pred. No. 9.2e-99;
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           276 ACAGGTATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 335
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Db
                  479 TTCAAAGAT-GGCATTTCCCCCCAATGAAATACACAAGTAAACATTC 523
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RESULT 12
US-10-251-661-7
; Sequence 7, Application US/10251661
; Publication No. US20030166555A1
; GENERAL INFORMATION:
     APPLICANT: Alberini, Cristina M.
     APPLICANT: Bear, Mark F.
     TITLE OF INVENTION: Methods and Compositions for Regulating
     TITLE OF INVENTION: Memory Consolidation
     FILE REFERENCE: 3499.1001-003
     CURRENT APPLICATION NUMBER: US/10/251,661
     CURRENT FILING DATE: 2002-09-20
     PRIOR APPLICATION NUMBER: 60/193,614
     PRIOR FILING DATE: 2000-03-31
     PRIOR APPLICATION NUMBER: PCT/US01/10661
     PRIOR FILING DATE: 2001-04-02
     NUMBER OF SEQ ID NOS: 12
     SOFTWARE: FastSEQ for Windows Version 4.0
  SEQ ID NO 7
       LENGTH: 612
       TYPE: DNA
       ORGANISM: Homo sapiens
       FEATURE:
       NAME/KEY: CDS
       LOCATION: (151)...(564)
US-10-251-661-7
   Query Match
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   Best Local Similarity
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                  121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
Qу
                         367 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 426
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                  Qy
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RESULT 13
US-09-852-261-11
; Sequence 11, Application US/09852261
; Patent No. US20020083477A1
; GENERAL INFORMATION:
 APPLICANT: GOLDSPINK, GEOFFREY
 APPLICANT: TERENGHI, GIORGIO
  TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
  FILE REFERENCE: 117-351
  CURRENT APPLICATION NUMBER: US/09/852,261
  CURRENT FILING DATE: 2001-05-10
  PRIOR APPLICATION NUMBER: GB 0011278.9
  PRIOR FILING DATE: 2000-05-10
  NUMBER OF SEQ ID NOS: 14
  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
   LENGTH: 487
   TYPE: DNA
   ORGANISM: Rattus sp.
US-09-852-261-11
                   50.1%; Score 262; DB 9; Length 487;
 Query Match
 Best Local Similarity 74.7%; Pred. No. 1.5e-75;
 Matches 396; Conservative 0; Mismatches 75; Indels
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          61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120
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          121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
Db
       Qу
          181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
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          241 ATGCCCAAGACTCAG----- 255
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US-09-852-261-9
; Sequence 9, Application US/09852261
; Patent No. US20020083477A1
; GENERAL INFORMATION:
  APPLICANT: GOLDSPINK, GEOFFREY
  APPLICANT: TERENGHI, GIORGIO
  TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
  FILE REFERENCE: 117-351
  CURRENT APPLICATION NUMBER: US/09/852,261
  CURRENT FILING DATE: 2001-05-10
  PRIOR APPLICATION NUMBER: GB 0011278.9
  PRIOR FILING DATE: 2000-05-10
  NUMBER OF SEQ ID NOS: 14
  SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 9
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   ORGANISM: Homo sapiens
US-09-852-261-9
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Db
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Qу
           61 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
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Qу
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        Qу
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RESULT 15
US-10-238-114-1
; Sequence 1, Application US/10238114
; Publication No. US20030100073A1
; GENERAL INFORMATION:
; APPLICANT: Merial
; APPLICANT: ANDREONI , Christine Michele
  TITLE OF INVENTION: IGF-1 AS FELINE VACCINE ADJUVANT, IN PARTICULAR AGAINST
FELINE RETROVIRUS
  FILE REFERENCE: 454313-3165.1
  CURRENT APPLICATION NUMBER: US/10/238,114
  CURRENT FILING DATE: 2002-09-10
  PRIOR APPLICATION NUMBER: FR 01 11736
  PRIOR FILING DATE: 2001-09-11
  PRIOR APPLICATION NUMBER: US 60/318,666
  PRIOR FILING DATE: 2001-09-12
  NUMBER OF SEQ ID NOS: 20
  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
   LENGTH: 462
   TYPE: DNA
   ORGANISM: Felis catus
US-10-238-114-1
                     43.6%; Score 228; DB 15; Length 462;
 Query Match
 Best Local Similarity 92.3%; Pred. No. 2.3e-64;
                                                     0; Gaps
                                         20; Indels
                                                               0;
 Matches 240; Conservative 0; Mismatches
          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGGAGAC 60
Qv
           145 GGACCAGAGACGCTCTGTGGGGCTGAGTTGGTGGACGCTCTTCAGTTCGTGTGGAGAC 204
Db
         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
Qy
           205 AGGGGTTTTTATTTCAACAAGCCCACGGGGTATGGCTCCAGCAGTCGGAGGGCACCTCAG 264
Db
        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
Qy
            265 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGCGGCTAGAGATGTAC 324
Db
        Qy
            325 TGTGCACCCCTCAAGCCTGCCAAGTCTGCCCGCTCAGTCCGTGCTCAGCGCCACACTGAC 384
Db
        241 ATGCCCAAGACTCAGAAGTA 260
Qy
            1111111
        385 ATGCCCAAGGCTCAGAAGGA 404
Db
Search completed: December 13, 2003, 11:56:48
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Job time : 235.512 secs